

6800 chip human RA PBMC

name	qualifier	GeneSpring qualifier	Patients called "p">4	#"p" (RA)	Avg Freq - RA	Normals called "p">6 (Normal)	#"p" (RA)	Avg Freq Normals	Ratio	Fold Change	Symbol	Chromosome	Description	function
MR110000	D64154 at	D64154	fail	4		PASS	13	9.77	Normal	Normal	RAC2	22q12-q13.2	Mr 110,000 antigen	ras-related C3 botulinum toxin
RAC2	M64595_at	M64595	fail	3		PASS	13	19.85	Normal	Normal			ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)
J03263 s at	J03263 s at	J03263	fail	3		PASS	13	9.23	Normal	Normal	LAMP1		thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V)	membrane glycoprotein
TBXAS1	M80647_at	M80647	fail	4		PASS	12	17.42	Normal	Normal	TBXAS1	7q34-q35	thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V)	thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V)
ALDR1	J04794 at	J04794	fail	4		PASS	12	14.42	Normal	Normal	ALDR1		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl- Coenzyme A thiolase/enoyl- Coenzyme A hydratase (trifunctional protein), alpha su subunit	aldehyde reductase (EC 1.1.1.2)
HADHA	D16480_at	D16480	fail	2		PASS	12	16.33	Normal	Normal	HADHA	2p23	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl- Coenzyme A thiolase/enoyl- Coenzyme A hydratase (trifunctional protein), alpha su subunit	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl- Coenzyme A thiolase/enoyl- Coenzyme A hydratase (trifunctional protein), alpha subunit
M13929 s at	M13929 s at	M13929	fail	1		PASS	12	9.33	Normal	Normal	MYC		c-myc-P64 protein	ORF 114; putative
HLK1	U40462_at	U40462	fail	1		PASS	12	6.42	Normal	Normal	hik-1		ikaros/Lyf-1 homolog	similar to mouse Lyf-1, encoded by GenBank Accession Number S74708; similar to mouse Ikaros DNA-binding protein, Swiss-Prot Accession Number Q03267
MANA2	D63998 at	D63998	fail	1		PASS	12	5.25	Normal	Normal	MANA2	5	mannosidase, alpha type II	mannosidase, alpha type II
ITBA2	X92896 at	X92896	fail	0		PASS	12	6.42	Normal	Normal	ITBA2			
PPP1R2	U88111 at	U88111	fail	0		PASS	12	5.17	Normal	Normal	PPP1R2		protein phosphatase inhibitor 2	
LCP2	U93049_at	U93049	fail	3		PASS	11	11.82	Normal	Normal	FYB		FYN-binding protein (FYB- 120/130)	FYN-binding protein (FYB- 120/130)
PCNA	J05614 at	J05614	fail	3		PASS	11	11.73	Normal	Normal			RNA polymerase II	
POLR2B	L37127 at	L37127	fail	2		PASS	11	13.27	Normal	Normal				
DG	HG1872-HT	HG1872-H	fail	2		PASS	11	10.55	Normal	Normal				
MEL	X56741 at	X56741	fail	2		PASS	11	7.82	Normal	Normal	rab8		rab8 small GTP binding	
U09178 s at	U09178 s at	U09178	fail	2		PASS	11	6.91	Normal	Normal	DPYD	1p22	dihydropyrimidine dehydrogenase	dihydropyrimidine dehydrogenase
CALM	U45976 at	U45976	fail	2		PASS	11	6.91	Normal	Normal	CALM		CALM	
TLE4	M99439_at	M99439	fail	2		PASS	11	5.73	Normal	Normal	TLE4		transducin-like enhancer protein	transducin-like enhancer of split 4, homolog of Drosophila E(sp1)
HSPA4	L12723 at	L12723	fail	2		PASS	11	5.45	Normal	Normal	HSPA4	5q31.1-q31.2	heat shock 70kD protein 4	heat shock 70kD protein 4
NUCP40	U86602_at	U86602	fail	2		PASS	11	5.09	Normal	Normal			nucleolar protein p40	cell proliferation-associated protein
E_CIT987SK	U91327 at	U91327	fail	1		PASS	11	5.82	Normal	Normal	99D8.1		T-complex protein 1, Beta subunit (TCP-1-BETA)	
FRAP	L34075_at	L34075	fail	1		PASS	11	5.73	Normal	Normal	FRAP1	1p36.2	FKBP-rapamycin associated protein	FK506 binding protein 12- rapamycin associated protein 1
EIF2G	L19161_at	L19161	fail	1		PASS	11	5.64	Normal	Normal	EIF2S3	Xp22.2-p22.1	eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD)	eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD)
P_E46	Z93784_at	Z93784	fail	1		PASS	11	5.36	Normal	Normal	dJ398C22.1		dJ398C22.1	E46-like contains exons 2-9 continues in Z84478
UCHL3	M30496_at	M30496	fail	1		PASS	11	4.27	Normal	Normal				ubiquitin carboxyl-terminal hydrolase

RPA1	M63488_at	M63488	fail	0	PASS	11	0	7.45	Normal	Normal	RPA1	17	replication protein A1 (70kD)	replication protein A1 (70kD)
RINF	HG511-HT5	HG511-HT5	fail	0	PASS	11	0	5.36	Normal	Normal				
M26041_s_a	M26041_s_a	M26041	fail	3	PASS	10	3	20.70	Normal	Normal	HLA-DQA1	6p21.3	major histocompatibility complex, class II, DQ alpha 1	major histocompatibility complex, class II, DQ alpha 1
K91_PCSK	D42053_at	D42053	fail	2	PASS	10	2	6.70	Normal	Normal	SIP	16	site-1 protease (subtilisin-like, sterol-regulated, cleaves sterol regulatory element binding proteins)	site-1 protease (subtilisin-like, sterol-regulated, cleaves sterol regulatory element binding proteins)
KCNQ1	U40990_at	U40990	fail	2	PASS	10	2	6.70	Normal	Normal	KVLQT1		voltage gated potassium	
GALC	L23116_at	L23116	fail	2	PASS	10	2	5.40	Normal	Normal	GALC	14q31	galactosylceramidase (Krabbe disease)	galactosylceramidase (Krabbe disease)
KPNB3	U72761_at	U72761	fail	2	PASS	10	2	5.40	Normal	Normal	KPNB3		karyopherin (importin) beta 3	karyopherin (importin) beta 3
DR1	M97388_at	M97388	fail	2	PASS	10	2	5.30	Normal	Normal	DR1	1p22.1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	down-regulator of transcription 1, TBP-binding (negative cofactor 2)
RFC4	M87339_at	M87339	fail	2	PASS	10	2	5.20	Normal	Normal	RFC4	3q27	replication factor C (activator 1) 4	replication factor C (activator 1) 4
BIOBM	AFFX-BioB	AFFX-BioB	fail	1	PASS	10	1	7.20	Normal	Normal				
UBE2D1	HG3344-HT5	HG3344-HT5	fail	1	PASS	10	1	6.50	Normal	Normal				
MANA2	L28821_at	L28821	fail	1	PASS	10	1	6.30	Normal	Normal	MAN2A2	15q25	alpha mannosidase II isozyme	mannosidase, alpha, class 2A, member 2
CAMKA2	U81554_at	U81554	fail	1	PASS	10	1	5.50	Normal	Normal	CAMK2G	10q22	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma
HG2797-HT5	HG2797-HT5	HG2797-HT5	fail	1	PASS	10	1	5.20	Normal	Normal				
POH1	U86782_at	U86782	fail	1	PASS	10	1	5.00	Normal	Normal	POH1		26S proteasome-associated pad1 homolog	human homolog of fission yeast pad1
GZMM	HG3104-HT5	HG3104-HT5	fail	0	PASS	10	0	16.20	Normal	Normal				
BAP	U72512_at	U72512	fail	3	PASS	9	3	13.56	Normal	Normal				
ESD	D28416_at	D28416	fail	3	PASS	9	3	10.89	Normal	Normal				
KO1160_s_at	KO1160_s_at	KO1160	fail	3	PASS	9	3	10.00	Normal	Normal				
U45878_s_at	U45878_s_at	U45878	fail	3	PASS	9	3	9.22	Normal	Normal				
RPS4Y	M58459_at	M58459	fail	2	PASS	9	2	44.67	Normal	Normal	RPS4Y	Yp11.3	inhibitor of apoptosis protein 1	HLAP-1
LTR	M92449_at	M92449	fail	2	PASS	9	2	9.89	Normal	Normal	PLT		ribosomal protein S4, Y-linked	ribosomal protein S4, Y-linked
FBP1	U05040_at	U05040	fail	2	PASS	9	2	7.67	Normal	Normal	FUBP		putative	putative
CD27	M63928_at	M63928	fail	2	PASS	9	2	7.44	Normal	Normal	TNFRSF7	12p13	FUSE-binding protein	far upstream element binding protein
FGFR1	U28811_at	U28811	fail	2	PASS	9	2	6.11	Normal	Normal	CFR-1		CD27 antigen	tumor necrosis factor receptor superfamily, member 7
PTPRA	M34668_at	M34668	fail	2	PASS	9	2	5.67	Normal	Normal	PTPRA	20p13	cysteine-rich fibroblast growth factor receptor	protein tyrosine phosphatase, receptor type, alpha polypeptide
U52191_s_at	U52191_s_at	U52191	fail	2	PASS	9	2	5.56	Normal	Normal	SMCY	Yq	SMC (mouse) homolog, Y chromosome	SMC (mouse) homolog, Y chromosome
U72935_cds3	U72935_cds3	U72935	fail	2	PASS	9	2	5.22	Normal	Normal	ATRX		putative DNA dependent ATPase and helicase	XH2; XNP; alternately spliced product 1; translation starts in exon 9
CBR	J04056_at	J04056	fail	2	PASS	9	2	4.89	Normal	Normal	CBR1	21q22.1	carboxyl reductase 1	carboxyl reductase 1
HSPB1	Z23090_at	Z23090	fail	1	PASS	9	1	12.56	Normal	Normal	HSPB1	7q	heat shock 27kD protein 1	heat shock 27kD protein 1
STAT1b	AFFX-HUM	AFFX-HUM	fail	1	PASS	9	1	7.00	Normal	Normal				
K129_RPT1	D50919_at	D50919	fail	1	PASS	9	1	4.89	Normal	Normal	KIAA0129			KIAA0129 gene product

CDK7	L20320_at	L20320	fail	1	PASS	9	1	4.89	Normal	Normal	CDK7	2p15-cen	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)
FABP5	M94856_at	M94856	fail	1	PASS	9	1	4.78	Normal	Normal	FABP5		fatty acid binding protein 5 (psoriasis-associated)	fatty acid binding protein 5 (psoriasis-associated)
ICSBP1	M91196_at	M91196	fail	0	PASS	9	0	8.33	Normal	Normal	ICSBP1		interferon consensus sequence binding protein 1	interferon consensus sequence binding protein 1
NMT1	M86707_at	M86707	fail	0	PASS	9	0	7.33	Normal	Normal	NMT1		N-myristoyltransferase 1	N-myristoyltransferase 1
RAB4	M28211_at	M28211	fail	0	PASS	9	0	5.11	Normal	Normal	RAB4	1q42-q43	RAB4, member RAS oncogene family	RAB4, member RAS oncogene family
ERPR1	M27826_at	M27826	fail	2	PASS	8	2	10.63	Normal	Normal			neutral protease large subunit	Xxx; putative
EV12A	M55267_at	M55267	fail	2	PASS	8	2	10.13	Normal	Normal	EV12A		EV12 protein	
H2BH f	Z80780_f at	Z80780	fail	1	PASS	8	1	9.88	Normal	Normal	H2BH/h		histone H2B	
TIP60	U74667_at	U74667	fail	0	PASS	8	0	7.25	Normal	Normal	TIP60		tat interactive protein	interacts with HIV1 Tat; similar to acetyltransferase; similar to yeast SAS2, SAS3 and human MOZ, encoded by GenBank Accession Numbers U14548, Z23261 and U47742, respectively; similar to sequence with GenBank Accession Number U40989
PHB	S85655_at	S85655	fail	0	PASS	8	0	6.63	Normal	Normal	PHB	17q21	prohibitin	prohibitin
EPHB4	U07695_at	U07695	fail	0	PASS	8	0	6.50	Normal	Normal	EPHB4	7	EphB4	EphB4
SNAP23	U55936_at	U55936	fail	0	PASS	8	0	6.00	Normal	Normal	SNAP23		synaptosomal-associated protein, 23kD	synaptosomal-associated protein, 23kD
D26155_s at	D26155_s at	D26155	fail	0	PASS	8	0	5.13	Normal	Normal	SMARCA2	9p24-p23	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
PRP4H	U48736_at	U48736	fail	0	PASS	8	0	5.00	Normal	Normal	PRP4		serine/threonine-protein kinase PRP4 homolog	serine/threonine-protein kinase PRP4 homolog
IL16	HG270-HT2	HG270-HT	fail	0	PASS	8	0	4.75	Normal	Normal				
E18CPGE	HG3991-HT4	HG3991-H	fail	4	PASS	7	4	30.57	Normal	Normal				
RORET	U90547_at	U90547	fail	4	PASS	7	4	12.14	Normal	Normal	RoRet		Ro/SSA ribonucleoprotein homolog	Ro/SSA ribonucleoprotein homolog
HMG1Y_ma	L17131_ma	L17131	fail	4	PASS	7	4	9.71	Normal	Normal	HMG1Y	6p	high-mobility group (nonhistone chromosomal) protein isoforms 1 and Y	high-mobility group (nonhistone chromosomal) protein isoforms 1 and Y
AFFX-BioDr	AFFX-BioDr	AFFX-BioDr	fail	2	PASS	7	2	12.29	Normal	Normal				
TXBP181	U33822_at	U33822	fail	1	PASS	7	1	9.86	Normal	Normal	MAD1L1	7p22	MAD1 (mitotic arrest deficient, yeast, homolog)-like 1	MAD1 (mitotic arrest deficient, yeast, homolog)-like 1
NUCB	U31342_at	U31342	fail	0	PASS	7	0	6.14	Normal	Normal			nucleobindin	nucleobindin
DPH2L	U34880_at	U34880	fail	0	PASS	7	0	6.00	Normal	Normal	DPH2L1	17p13.3	diphtheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 1	diphtheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 1
TRAP1	U12595_at	U12595	fail	0	PASS	7	0	5.71	Normal	Normal	TRAP1		tumor necrosis factor type 1 receptor associated protein	TNF type 1 receptor associated protein
X60003 s at	X60003 s at	X60003	fail	0	PASS	7	0	5.43	Normal	Normal	delta CREB			
20GCP_ma	X66114_ma	X66114	fail	0	PASS	7	0	5.43	Normal	Normal	SLC20A4	17p13.3	solute carrier family 20 (oxoglutarate carrier), member 4	solute carrier family 20 (oxoglutarate carrier), member 4
K196	D83780_at	D83780	fail	0	PASS	7	0	5.14	Normal	Normal	KIAA0196		KIAA0196 gene product	KIAA0196 gene product

Gene	Accession	Protein	Length	Weight	Charge	PI	Abundance	Function	Location	Notes
K52 SKI2P	D29641	SKI-2	7	0	0	0	0	cytochrome c oxidase subunit 1	cytochrome c oxidase subunit 1	
CUL4A	U58090	CUL4A	7	0	0	0	0	cytochrome c oxidase subunit 1	cytochrome c oxidase subunit 1	
E_23707	U79270	CUL4A	7	0	0	0	0	cytochrome c oxidase subunit 1	cytochrome c oxidase subunit 1	
BLK	S76617	BLK	7	0	0	0	0	lymphoid tyrosine kinase	lymphoid tyrosine kinase	
U69140_s_at	U69140	BLK	7	0	0	0	0	lymphoid tyrosine kinase	lymphoid tyrosine kinase	
ERPL1	X89211	HERV-L	7	0	0	0	0	Human Endogenous Retrovirus-Like elements (HERV-L) /pseudo	Human Endogenous Retrovirus-Like elements (HERV-L) /pseudo	
PRTK1	S76965	PRTK1	7	0	0	0	0	protein kinase inhibitor	protein kinase inhibitor	This sequence comes from Fig. 1B; PKI
X93511_s_at	X93511	SP-10	7	0	0	0	0	SP-10	SP-10	
MAGEP15	U19796	MTA1	7	0	0	0	0	metastasis associated 1	metastasis associated 1	
HG3148-HT3	HG3148-H	MTA1	7	0	0	0	0	metastasis associated 1	metastasis associated 1	
U35113_at	U35113	MTA1	7	0	0	0	0	metastasis associated 1	metastasis associated 1	
HG4120-HT4	HG4120-H	MTA1	7	0	0	0	0	metastasis associated 1	metastasis associated 1	
AVPR1B	L37112	AVPR1B	7	0	0	0	0	vasopressin V3 receptor	vasopressin V3 receptor	
ACRV1_ma	S65583	SP-10	7	0	0	0	0	SP-10	SP-10	
U57623_s_at	U57623	FABP3	7	0	0	0	0	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	
AACT_ma1	X68733	ACT	7	0	0	0	0	ACT	ACT	
D29675_s_at	D29675	KCNMA1	7	0	0	0	0	KCNMA1	KCNMA1	
SLO	U02632	KCNMA1	7	0	0	0	0	KCNMA1	KCNMA1	
MME	J03779	MME	7	0	0	0	0	MME	MME	
K246 NOTC	D87433	KCNMA1	7	0	0	0	0	KCNMA1	KCNMA1	
MDC	U83171	SCYA22	7	0	0	0	0	SCYA22	SCYA22	
M22403_s_at	M22403	GP1BA	7	0	0	0	0	GP1BA	GP1BA	
FSTRP	U06863	GP1BA	7	0	0	0	0	GP1BA	GP1BA	
PLCG2H	U45974	GP1BA	7	0	0	0	0	GP1BA	GP1BA	
PTPRN	L18983	PTPRN	7	0	0	0	0	PTPRN	PTPRN	
AQP9	AB006190	AQP9	7	0	0	0	0	AQP9	AQP9	

EFNB3	U66406_at	U66406	PASS	5	7.40	fail	0	5	Disease	EFNB3	17p13.1-p11.2	ephrin-B3	ephrin-B3
M87789_s at OC116	M87789_s at U45285_at	M87789 U45285	PASS PASS	8 9	118.00 31.44	PASS PASS	9 10	8 9	6.03 4.31			IgG specific 116-kDa vacuolar proton pump subunit	Anti-hepatitis A; putative ATPase, H+ transporting, 116kD
UBE1	M58028_at	M58028	PASS	9	46.44	PASS	13	9	4.11	UBE1	Xp11.23	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing)	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing)
TETTRL CSF3R	L11669_at M59820_at	L11669 M59820	PASS PASS	6 6	28.33 43.67	PASS PASS	11 7	6 6	3.95 3.77	ADD1 CSF3R	4p16.3 1p35-p34.3	adducin 1 (alpha) colony stimulating factor 3 receptor (granulocyte)	adducin 1 (alpha) colony stimulating factor 3 receptor (granulocyte)
IGF2	S73149_at	S73149	PASS	8	35.13	PASS	9	8	3.76	orf in intron 7 of insulin- like growth factor II gene			
18SRNAM 18SRNA3 PROTEIN_1 V01512_ma1 V01512	AFFX-HUM1 AFFX-HUM1 AFFX-HUM1 V01512_ma1 V01512	AFFX-HUN AFFX-HUN AFFX-HUN V01512_ma1 V01512	PASS PASS PASS PASS	6 9 9 9	28.67 46.89 51.44	PASS PASS PASS	7 11 13	6 9 9	3.72 3.71 3.69				v-fos FBJ murine osteosarcoma viral oncogene homolog
ETR101 DIA1	M62831_at M28713_at	M62831 M28713	PASS PASS	9 9	105.67 33.33	PASS PASS	13 12	9 9	3.68 3.67	ETR101 DIA1	19 22q13.31-qter	immediate early protein cytochrome b5 reductase	immediate early protein cytochrome b5 reductase
MX1	M33882_at	M33882	PASS	7	34.71	PASS	9	7	3.63	MX1	21q22.3	myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible protein p78)	myxovirus (influenza) resistance 1, homolog of murine (interferon- inducible protein p78)
SELPLG LFP40	U25936_at U72206_at	U25936 U72206	PASS PASS	9 5	75.89 33.40	PASS PASS	13 10	9 5	3.60 3.59	SELPLG LFP40	12q24 chr. 1	selectin P ligand guanine nucleotide regulatory factor	selectin P ligand guanine nucleotide regulatory factor
BB1	S82470_at	S82470	PASS	6	32.00	PASS	12	6	3.59	BB1			malignant cell expression-enhanced gene/tumor progression-enhanced gene; This sequence comes from Fig. 4A
LYSPHADA	U56417_at	U56417	PASS	9	26.33	PASS	11	9	3.58			lysophosphatidic acid acyltransferase-alpha	LPAA1-a; 1-acyl-sn-glycerol-3- phosphate acyltransferase; similar to sequence within class III MHC locus on chromosome 6 deposited in GenBank Accession Number U89336
HG4535-HT4 ZYX S71043_ma1 S71043	HG4535-HT4 X95735_at S71043_ma1 S71043	HG4535-H X95735 S71043_ma1 S71043	PASS PASS PASS	8 8 9	38.50 41.38 88.33	PASS PASS PASS	8 10 13	8 8 9	3.54 3.54 3.41	ZYX Ig<lt>alpha >2	7q32	zyxin immunoglobulin A heavy chain allotype 2	This sequence comes from Fig. 3; IgA2 H chain
HD ILK	L12392_at U40282_at	L12392 U40282	PASS PASS	9 9	22.33 29.22	PASS PASS	9 12	9 9	3.41 3.40	HD ILK	4p16.3 11p15.5-p15.4	huntingtin integrin-linked kinase	huntingtin (Huntington disease) integrin-linked kinase
PKM2 CD63_ma1	X56494_at X62654_ma1 X62654	X56494 X62654_ma1 X62654	PASS PASS	8 9	63.50 41.78	PASS PASS	13 13	8 9	3.38 3.37	PKM2 CD63	15q22-qter 12q12-q13	pyruvate kinase, muscle CD63 antigen (melanoma 1 antigen)	pyruvate kinase, muscle CD63 antigen (melanoma 1 antigen)
SA X62083_s at	M60922_at X62083_s at	M60922 X62083	PASS PASS	8 9	55.88 70.89	PASS PASS	12 13	8 9	3.37 3.35	FLOT2 FSH	17q11-q12	flotillin 2	flotillin 2

J03260_s_at	J03260_s_at	J03260	PASS	7	28.71	PASS	7	7	8.57	3.35	3.35	3.35	GNAZ	22q11.1-q11.2	guanaine nucleotide binding protein (G protein), alpha z polypeptide	guanaine nucleotide binding protein (G protein), alpha z polypeptide
CDC25	S78187_at	S78187	PASS	9	63.89	PASS	13	9	19.08	3.35	3.35	3.35	CDC25B	20p13	cell division cycle 25B	cell division cycle 25B
RELA	L19067_at	L19067	PASS	9	39.78	PASS	10	9	11.90	3.34	3.34	3.34			NF-kappa-B transcription factor subunit	putative
XQTP	D16469_at	D16469	PASS	9	31.67	PASS	11	9	9.55	3.32	3.32	3.32	ATP6S1	Xq28	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1
RAGE_cds1	U89336_cds1	U89336	PASS	9	71.78	PASS	13	9	21.69	3.31	3.31	3.31	HBX2		homeobox PBX2 gene	intron-exon boundaries identified by a contig of ESTs with GenBank Accession Numbers W76064, R59617, W72507
K154_ADTC	D63876_at	D63876	PASS	9	33.89	PASS	12	9	10.25	3.31	3.31	3.31	KIAA0154		KIAA0154 gene product is related to mouse gamma adaptin.	KIAA0154 gene product is related to mouse gamma adaptin.
PRSM1	U58048_at	U58048	PASS	8	18.63	PASS	9	8	5.67	3.29	3.29	3.29	PRSM1	16q24.3	protease, metallo, 1, 33kD	protease, metallo, 1, 33kD
ATP6C	M62762_at	M62762	PASS	9	69.67	PASS	13	9	21.23	3.28	3.28	3.28	ATP6C	16p13.3	ATPase, H+ transporting, lysosomal (vacuolar proton pump), 16kD	ATPase, H+ transporting, lysosomal (vacuolar proton pump), 16kD
NCF1	M55067_at	M55067	PASS	9	72.33	PASS	13	9	22.08	3.28	3.28	3.28	NCF1	7q11.23	neutrophil cytosolic factor 1	neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1)
K220	D86974_at	D86974	PASS	9	239.22	PASS	13	9	73.38	3.26	3.26	3.26	KIAA0220			
K109_CLAS1	D63475_at	D63475	PASS	8	45.88	PASS	13	8	14.15	3.24	3.24	3.24	CLAPM1	3q28	clathrin-associated/assembly/adaptor protein, medium 1	clathrin-associated/assembly/adaptor protein, medium 1
TSC2	L48546_at	L48546	PASS	9	30.44	PASS	7	9	9.43	3.23	3.23	3.23	TSC2	16p13.3	tuberous sclerosis 2	tuberous sclerosis 2
EDR2	U89278_at	U89278	PASS	8	25.25	PASS	12	8	7.83	3.22	3.22	3.22	EDR2		early development regulator 2 (homolog of polyhomeotic 2)	early development regulator 2 (homolog of polyhomeotic 2)
M34996_s_at	M34996_s_at	M34996	PASS	9	80.56	PASS	13	9	25.08	3.21	3.21	3.21	PNUTL1	22q11.2	cell surface glycoprotein	cell surface glycoprotein
U59632_s_at	U59632_s_at	U59632	PASS	9	97.22	PASS	13	9	30.54	3.18	3.18	3.18	USP11	Xp21.2-p11.2	ubiquitin carboxyl-terminal hydrolase, X-linked	ubiquitin carboxyl-terminal hydrolase, X-linked
UHX1	U44839_at	U44839	PASS	9	60.22	PASS	13	9	18.92	3.18	3.18	3.18	USP11	Xp21.2-p11.2	ubiquitin carboxyl-terminal hydrolase, X-linked	ubiquitin carboxyl-terminal hydrolase, X-linked
UROD	X89267_at	X89267	PASS	5	47.60	PASS	8	5	15.25	3.12	3.12	3.12			uroporphyrinogen decarboxylase	uroporphyrinogen decarboxylase
PLCB2	M95678_at	M95678	PASS	9	84.00	PASS	12	9	26.92	3.12	3.12	3.12	PLCB2	15q15	phospholipase C, beta 2	phospholipase C, beta 2
BST2	D28137_at	D28137	PASS	8	51.13	PASS	13	8	16.38	3.12	3.12	3.12	BST2	19p13.2	bone marrow stromal cell antigen 2	bone marrow stromal cell antigen 2
NFER2	S77763_at	S77763	PASS	9	32.33	PASS	11	9	10.36	3.12	3.12	3.12	nuclear factor erythroid 2 isoform f, transcription factor		nuclear factor erythroid 2 isoform f, transcription factor	basic leucine zipper protein; This sequence comes from Fig. 1; transcription factor fNF-E2
EBVIP	U19261_at	U19261	PASS	6	22.67	PASS	7	6	7.29	3.11	3.11	3.11			Epstein-Barr virus-induced protein	EBV induced protein
28SRNAM	AFFX-M278	AFFX-M278	PASS	5	91.00	PASS	7	5	29.29	3.11	3.11	3.11				
GSTZ1	U86529_at	U86529	PASS	9	25.56	PASS	11	9	8.27	3.09	3.09	3.09	GSTZ1	14q24.3	glutathione S-transferase Zeta 1	glutathione S-transferase Zeta 1
CD151	D29963_at	D29963	PASS	8	31.13	PASS	7	8	10.14	3.07	3.07	3.07	CD151	11p15.5	CD151 antigen	CD151 antigen
SAT_ma1	U40369_ma1	U40369	PASS	9	37.67	PASS	13	9	12.31	3.06	3.06	3.06	SAT	Xp22.1	spermidine/spermine N1-acetyltransferase	spermidine/spermine N1-acetyltransferase

CLU	M63379_at	M63379	PASS	9	222.78	PASS	13	9	72.85	3.06	3.06	3.06	CLU	8p21-p12	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)
HMG1	D63874_at	D63874	PASS	9	83.22	PASS	13	9	27.31	3.05	3.05	3.05	HMG1	13q12	high-mobility group (nonhistone chromosomal) protein 1
DEFA1	M26602_at	M26602	PASS	7	185.43	PASS	11	7	61.09	3.04	3.04	3.04	DEFA1	8p23.2-p23.1	defensin, alpha 1, myeloid-related sequence
FCGR1A	J04162_at	J04162	PASS	9	46.56	PASS	13	9	15.38	3.03	3.03	3.03	FCGR3A	1q23	Fc fragment of IgG, low affinity IIIa, receptor for (CD16)
M32304_s_a	M32304_s_a	M32304	PASS	8	26.75	PASS	13	8	8.85	3.02	3.02	3.02	TIMP2	17q25	tissue inhibitor of metalloproteinase 2
LSP1	M33552_at	M33552	PASS	9	48.11	PASS	13	9	15.92	3.02	3.02	3.02	LSP1		lymphocyte-specific protein 1 (LSP1)
U83239_s_at	U83239_s_at	U83239	PASS	6	34.33	PASS	11	6	11.36	3.02	3.02	3.02			CC chemokine STCP-1
GSTH	U90313_at	U90313	PASS	9	43.22	PASS	13	9	14.31	3.02	3.02	3.02	GSTTLP28		glutathione-S-transferase like
IGLT1	U82275_at	U82275	PASS	8	27.88	PASS	12	8	9.25	3.01	3.01	3.01			immunoglobulin-like transcript 1
NRGN_ma1	X99076_ma1	X99076	PASS	9	230.11	PASS	13	9	76.54	3.01	3.01	3.01	NRGN		neurogranin
UBA52	M26880_at	M26880	PASS	9	198.00	PASS	13	9	66.31	2.99	2.99	2.99	UBA52	19p13.1-p12	ubiquitin A-52 residue ribosomal protein fusion product 1
TMEM1	D26579_at	D26579	PASS	9	31.56	PASS	13	9	10.62	2.97	2.97	2.97	ADAM8	10q26.3	a disintegrin and metalloprotease domain 8
GPI	K03515_at	K03515	PASS	9	35.78	PASS	13	9	12.08	2.96	2.96	2.96	GPI	19q13.1	glucose phosphate isomerase
TYL	X99688_at	X99688	PASS	9	23.44	PASS	12	9	7.92	2.96	2.96	2.96	TYL		tyrosine phosphatase
UBE1L	L13852_at	L13852	PASS	9	54.78	PASS	13	9	18.62	2.94	2.94	2.94	UBE1L	3p21	ubiquitin-activating enzyme E1, like
KRT1_ma1	M98776_ma1	M98776	PASS	7	19.29	PASS	9	7	6.56	2.94	2.94	2.94	KRT1		keratin 1
K45_YKL	D28476_at	D28476	PASS	9	27.44	PASS	12	9	9.33	2.94	2.94	2.94	TRIP12		thyroid hormone receptor interactor 12
HCFC1	L20010_at	L20010	PASS	8	26.13	PASS	13	8	8.92	2.93	2.93	2.93			
SLC9A1	S68616_at	S68616	PASS	5	20.20	PASS	10	5	6.90	2.93	2.93	2.93	SLC9A1	1p36.1-p35	Na+/H+ exchanger NHE-1 isoform
SCYA5	M21121_at	M21121	PASS	9	156.78	PASS	13	9	53.69	2.92	2.92	2.92	SCYA5	17q11.2-q12	small inducible cytokine A5 (RANTES)
PRKMK3	D87116_at	D87116	PASS	9	32.89	PASS	11	9	11.27	2.92	2.92	2.92	PRKMK3	17q11.2	protein kinase, mitogen-activated, kinase 3 (MAP kinase kinase 3)
CCND3	M92287_at	M92287	PASS	9	68.33	PASS	13	9	23.62	2.89	2.89	2.89	CCND3	6p21	cyclin D3
SMN1_ma2	U80017_ma2	U80017	PASS	8	18.38	PASS	11	8	6.36	2.89	2.89	2.89	bt2p44		basic transcription factor 2, p44
PLCG2H	U45975_at	U45975	PASS	6	23.50	PASS	7	6	8.14	2.89	2.89	2.89			phosphatidylinositol (4,5)bisphosphate 5-phosphatase homolog
X74874_ma1	X74874_ma1	X74874	PASS	8	19.75	PASS	13	8	6.85	2.88	2.88	2.88			RNA polymerase II largest subunit
M36118_s_at	M36118_s_at	M36118	PASS	8	33.63	PASS	12	8	11.67	2.88	2.88	2.88	GZMB	14q11.2	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)

IMPDH1	J05272_at	J05272	PASS	9	31.44	PASS	13	9	10.92	2.88	2.88	IMPDH1	7q31.3-q32	IMP (inosine monophosphate) dehydrogenase 1
S40719 s at	S40719 s at	S40719	PASS	9	19.89	PASS	11	9	6.91	2.88	2.88	GFAP	17q21	glial fibrillary acidic protein
NAP1L4	U77456 at	U77456	PASS	6	29.50	PASS	12	6	10.25	2.88	2.88			nucleosome assembly protein 2
E ZNF162	L49380 at	L49380	PASS	9	46.44	PASS	13	9	16.15	2.88	2.88	ZNF162	11q13	zinc finger protein 162
S100A12	D83657_at	D83657	PASS	9	65.44	PASS	13	9	22.77	2.87	2.87			CAAF1 (calcium-binding protein in amniotic fluid 1)
K56	D29954 at	D29954	PASS	8	18.88	PASS	7	8	6.57	2.87	2.87	KIAA0056		CHLI protein
E DDX11	U75968 at	U75968	PASS	9	20.56	PASS	12	9	7.17	2.87	2.87	CHLR1		150 kDa oxygen-regulated protein ORP150
ORP150	U65785_at	U65785	PASS	9	33.67	PASS	12	9	11.75	2.87	2.87			ADP-ribosylation factor 5
ARF5	M57567 at	M57567	PASS	8	46.00	PASS	13	8	16.15	2.85	2.85	ARF5	7q31.3	protease inhibitor 6 (placental thrombin inhibitor)
S69272 s at	S69272 s at	S69272	PASS	9	24.67	PASS	13	9	8.69	2.84	2.84	P16	6p25	MAP-kinase activating death domain
AB002356 s	AB002356 s	AB002356	PASS	9	31.67	PASS	12	9	11.17	2.84	2.84	MADD	11p11.21-p11.22	regulator of G-protein signalling 2, 24kD
CSF1	HG1155-HT4	HG1155-H	PASS	8	27.63	PASS	9	8	9.78	2.83	2.83			uridine phosphorylase
RGS2	L13391_at	L13391	PASS	9	60.33	PASS	13	9	21.38	2.82	2.82	RGS2	1q31	2',3'-cyclic-nucleotide 3'-phosphodiesterase (CNPI)
UP	X90858 at	X90858	PASS	9	21.44	PASS	13	9	7.62	2.82	2.82	UP	7	cytidine deaminase
K250	D87437 at	D87437	PASS	9	19.33	PASS	9	9	6.89	2.81	2.81	KIAA0250		FAST kinase
CNP_cds1	D13146_cds1	D13146	PASS	9	49.89	PASS	13	9	17.85	2.80	2.80			c-src tyrosine kinase
CDA	L27943 at	L27943	PASS	6	32.33	PASS	10	6	11.60	2.79	2.79	CDA	1p36.2-p35	D component of complement (adipsin)
FAST	X86779 at	X86779	PASS	9	20.33	PASS	10	9	7.30	2.79	2.79	fast		hepatitis C-associated microtubular aggregate protein p44
X59932 s at	X59932 s at	X59932	PASS	9	62.44	PASS	13	9	22.46	2.78	2.78	CSK	15q23-q25	CD33 antigen (gp67)
MAZ	M94046 at	M94046	PASS	9	29.67	PASS	13	9	10.69	2.77	2.77			14-3-3 protein eta clam
DF	M84526_at	M84526	PASS	5	43.40	PASS	12	5	15.67	2.77	2.77	DF		clathrin, light polypeptide (Lca)
PRKM3	D28915_at	D28915	PASS	7	16.00	PASS	10	7	5.80	2.76	2.76			myeloid cell leukemia sequence 1 (BCL2-related)
CD33	M23197 at	M23197	PASS	8	21.00	PASS	13	8	7.62	2.76	2.76	CD33	19q13.3	tumor necrosis factor receptor superfamily, member 1B
D78577 s at	D78577 s at	D78577	PASS	9	85.67	PASS	13	9	31.08	2.76	2.76			guanine nucleotide binding protein 10
BRF2	X78992 at	X78992	PASS	8	64.88	PASS	13	8	23.54	2.76	2.76	ERF-2		polymerase (RNA) II (DNA directed) polypeptide E (25kD)
CLTA	M20471 at	M20471	PASS	9	73.56	PASS	13	9	26.69	2.76	2.76	CLTA	12q23-q24	KIAA0050 gene product
HG2868-HT1	HG2868-HT1	HG2868-H	PASS	7	18.57	PASS	12	7	6.75	2.75	2.75			transforming growth factor-beta
MCL1	L08246_at	L08246	PASS	9	88.67	PASS	13	9	32.23	2.75	2.75	MCL1	1q21	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)
S100A11	D38583 at	D38583	PASS	9	81.00	PASS	13	9	29.54	2.74	2.74			adenosine monophosphate deaminase 2 (isoform L)
TNFR2	M32315_at	M32315	PASS	9	67.44	PASS	13	9	24.62	2.74	2.74	TNFRSF1B	1p36.3-p36.2	
GNG10	U31383_at	U31383	PASS	9	18.33	PASS	13	9	6.69	2.74	2.74	GNG10		
D38251 s at	D38251 s at	D38251	PASS	8	30.75	PASS	13	8	11.23	2.74	2.74	POLR2E	19p13.3	
K50 K41	D30758 at	D30758	PASS	9	61.89	PASS	13	9	22.62	2.74	2.74	KIAA0050		
M38449 s at	M38449 s at	M38449	PASS	6	33.50	PASS	8	6	12.25	2.73	2.73	TGF-beta		
GT197	L38932_at	L38932	PASS	9	40.33	PASS	13	9	14.77	2.73	2.73	BECN1		
AMPD2_cds1	M91029_cds1	M91029	PASS	9	30.33	PASS	13	9	11.15	2.72	2.72	AMPD2	1p13.3	

K226	D86979_at	D86979	PASS	9	20.56	PASS	13	9	7.85	2.62	2.62	KIAA0226			KIAA0226 gene product
BTN_mal	U97502_mal	U97502	PASS	6	16.50	PASS	13	6	6.31	2.62	2.62	BT3.3			butyrophilin
L32831_s_at	L32831_s_at	L32831	PASS	5	18.00	PASS	9	5	6.89	2.61	2.61				G protein-coupled receptor GPR3
FKBP4	M88279_at	M88279	PASS	9	23.11	PASS	13	9	8.85	2.61	2.61	FKBP4			FK506-binding protein 4 (59kD)
CTSD	M63138_at	M63138	PASS	9	82.89	PASS	12	9	31.75	2.61	2.61	CTSD	11p15.5		cathepsin D (lysosomal aspartyl protease)
HG2815-HT4	HG2815-HT4	HG2815-HT4	PASS	9	360.22	PASS	13	9	138.00	2.61	2.61				
L13939_s_at	L13939_s_at	L13939	PASS	8	24.88	PASS	13	8	9.54	2.61	2.61	ADTBI	22q12		adaptin, beta 1 (beta prime)
AOAH	M62840_at	M62840	PASS	8	27.50	PASS	9	8	10.56	2.61	2.61	AOAH	7p14-p12		acyloxycyl hydrolase (neutrophil)
TPR1	U46570_at	U46570	PASS	9	41.67	PASS	13	9	16.08	2.59	2.59	TTC1	5q32-q33.2		tetratricopeptide repeat domain 1
TUBA1	X01703_at	X01703	PASS	9	37.67	PASS	13	9	14.54	2.59	2.59				alpha-tubulin
CSR1	M62505_at	M62505	PASS	8	25.00	PASS	12	8	9.67	2.59	2.59	CSR1	19q13.3-q13.4		complement component 5 receptor 1 (C5a ligand)
U43185_s_at	U43185_s_at	U43185	PASS	9	27.56	PASS	12	9	10.67	2.58	2.58	STAT5A	17q11.2		signal transducer and activator of transcription 5A
AARS	D32050_at	D32050	PASS	8	19.38	PASS	12	8	7.50	2.58	2.58	AARS	16q22		alanyl-tRNA synthetase
SREBF1	U00968_at	U00968	PASS	6	24.67	PASS	7	6	9.57	2.58	2.58	SREBF1	17p11.2		sterol regulatory element binding transcription factor 1
GIP2	M13755_at	M13755	PASS	7	30.71	PASS	13	7	11.92	2.58	2.58	ISG15	1		interferon-stimulated protein, 15 kDa
BCAT2	U62739_at	U62739	PASS	9	18.78	PASS	10	9	7.30	2.57	2.57	BCAT2	19		branched chain aminotransferase 2, mitochondrial
DCTD	L39874_at	L39874	PASS	8	26.38	PASS	11	8	10.27	2.57	2.57	DCTD			dCMP deaminase
K15_PPM1A	D13640_at	D13640	PASS	9	29.00	PASS	12	9	11.33	2.56	2.56	KIAA0015			KIAA0015 gene product
RTP	D87953_at	D87953	PASS	9	39.56	PASS	13	9	15.46	2.56	2.56	GC4			RTP
PXN	U14588_at	U14588	PASS	9	39.11	PASS	13	9	15.31	2.55	2.55	PXN	12q24		paxillin
KAP1_TIF1B	U95040_at	U95040	PASS	9	44.00	PASS	13	9	17.31	2.54	2.54				hKAP1/TIF1B
NRBTk	L20773_at	L20773	PASS	9	25.56	PASS	13	9	10.08	2.54	2.54				
AJ000099_s	AJ000099_s	AJ000099_s	PASS	7	28.57	PASS	11	7	11.27	2.53	2.53	HYAL2	3p21.3		hyaluronoglucosaminidase 2
BZRP	L21954_at	L21954	PASS	9	127.89	PASS	13	9	50.46	2.53	2.53	BZRP	22q13.3		benzodiazepine receptor (peripheral)
HUK5	U67963_at	U67963	PASS	9	18.89	PASS	11	9	7.45	2.53	2.53	HUK5			lysophospholipase homolog
YF5	U84569_at	U84569	PASS	8	24.88	PASS	13	8	9.85	2.53	2.53				YF5
															similar to A2 encoded by GenBank Accession Number U84570 and to sequence with GenBank Accession Number AC000020
STX5A	U26648_at	U26648	PASS	6	21.33	PASS	9	6	8.44	2.53	2.53	STX5A			syntaxin 5A
X65784_s_at	X65784_s_at	X65784	PASS	8	21.88	PASS	12	8	8.67	2.52	2.52	CMAR	16q		cell matrix adhesion regulator
SFCC13	L10910_at	L10910	PASS	9	16.11	PASS	13	9	6.38	2.52	2.52	CCI.3	20		splicing factor (CCI.3)
K79_CHR7	D38555_at	D38555	PASS	9	21.33	PASS	10	9	8.50	2.51	2.51	KIAA0079	10		Sec24p, S. Cerevisiae, homolog of of
E_A9A2BRE	U00952_at	U00952	PASS	5	17.80	PASS	10	5	7.10	2.51	2.51				
LAG2	M85276_at	M85276	PASS	9	138.22	PASS	13	9	55.15	2.51	2.51	NKG5			NKG5 protein
M16750_s_at	M16750_s_at	M16750	PASS	9	34.89	PASS	13	9	13.92	2.51	2.51	PIM1	6p21		pim-1 oncogene
K120_NP25	D21261_at	D21261	PASS	9	278.78	PASS	13	9	111.31	2.50	2.50	TAGLN2	1q21-q25		transgelin 2
PRKACG	U42412_at	U42412	PASS	8	16.38	PASS	11	8	6.55	2.50	2.50	PRKAG1	12q12-q14		protein kinase, AMP-activated, gamma 1 non-catalytic subunit

OS9	U41635_at	U41635	PASS	9	58.56	PASS	13	9	24.23	2.42	2.42		OS-9 precursor	ubiquitously expressed in human tissues and amplified in sarcomas
RPS6KA2	L07597_at	L07597	PASS	9	28.78	PASS	12	9	11.92	2.41	2.41	RPS6KA1	3	ribosomal protein S6 kinase, 90kD, polypeptide 1
IFNG	L07633_at	L07633	PASS	9	84.33	PASS	13	9	34.92	2.41	2.41	PSME1	14q11.2	interferon-gamma
FRAPL	L37033_at	L37033	PASS	8	29.38	PASS	11	8	12.18	2.41	2.41	FKBP38		FK-506 binding protein homologue
CES1	L07765_at	L07765	PASS	7	15.43	PASS	10	7	6.40	2.41	2.41	CES1	16q13-q22.1	carboxylesterase 1 (monocyte/macrophage serine esterase 1)
X56681 s at	X56681 s at	X56681	PASS	9	114.44	PASS	13	9	47.54	2.41	2.41	JUND	19p13.2	jun D proto-oncogene
HDLBP	M64098_at	M64098	PASS	8	20.00	PASS	13	8	8.31	2.41	2.41	HBP		high density lipoprotein binding protein
ECGF1 ma3	U62317 ma3	U62317	PASS	9	66.22	PASS	13	9	27.54	2.40	2.40			arylsulfatase A
K140	D50930_at	D50930	PASS	8	18.13	PASS	11	8	7.55	2.40	2.40	KIAA0140		hypothetical protein 384D8.2
HG4541-HT4	HG4541-HT4	HG4541-HT4	PASS	9	41.56	PASS	13	9	17.31	2.40	2.40			KIAA0140 gene product
ARP	M83751 at	M83751	PASS	9	21.22	PASS	13	9	8.85	2.40	2.40	ARP		putative
HG417-HT4	HG417-HT4	HG417-HT4	PASS	9	71.33	PASS	13	9	29.77	2.40	2.40			arginine-rich protein
STM	U20499_at	U20499	PASS	9	20.33	PASS	12	9	8.50	2.39	2.39	SULT1A3	16p11.2	thermolabile phenol sulfotransferase
NP	K02574 at	K02574	PASS	8	32.88	PASS	13	8	13.77	2.39	2.39	NP		nucleoside phosphorylase
GLA	X14448 at	X14448	PASS	9	20.56	PASS	13	9	8.62	2.39	2.39			alpha-D-galactosidase A
ARNP	M74002_at	M74002	PASS	9	20.00	PASS	13	9	8.38	2.39	2.39	SFRS11	1p21-p34	splicing factor, arginine/serine-rich 11
K168	D79990 at	D79990	PASS	9	29.33	PASS	13	9	12.31	2.38	2.38	KIAA0168		KIAA0168 gene product
SUPT4H1	U43923_at	U43923	PASS	8	21.63	PASS	12	8	9.08	2.38	2.38	SUPT4H1	17q21-q23	suppressor of Ty (S.cerevisiae) 4 homolog 1
K174	D79996 at	D79996	PASS	9	28.56	PASS	13	9	12.00	2.38	2.38	KIAA0174		KIAA0174 gene product
DCT	U49785 at	U49785	PASS	9	24.89	PASS	13	9	10.46	2.38	2.38	DDT	22q11.2	D-dopachrome tautomerase
CLP36	U90878_at	U90878	PASS	9	26.56	PASS	12	9	11.17	2.38	2.38	CLIM1	10q22-q27	carboxyl terminal LIM domain protein 1
LAMP5	U51240_at	U51240	PASS	9	146.89	PASS	13	9	61.77	2.38	2.38	LAPTM5		lysosomal-associated multitransmembrane protein
NK4	M59807 at	M59807	PASS	9	116.67	PASS	13	9	49.15	2.37	2.37	NK4	16p13.3	natural killer cell transcript 4
K223_COSZ	D86976_at	D86976	PASS	9	103.11	PASS	13	9	43.46	2.37	2.37	KIAA0223		natural killer cell transcript 4 similar to C.elegans protein (Z37093)
B94	M92357 at	M92357	PASS	9	27.00	PASS	13	9	11.38	2.37	2.37			B94 protein
SPARC	J03040_at	J03040	PASS	9	57.78	PASS	13	9	24.38	2.37	2.37	SPARC	5q31-q33	secreted protein, acidic, cysteine-rich (osteonectin)
PPCB	M22960_at	M22960	PASS	9	83.44	PASS	13	9	35.23	2.37	2.37	PPGB	20q13.1	protective protein for beta-galactosidase
MX2	M30818_at	M30818	PASS	9	20.56	PASS	13	9	8.69	2.36	2.36	MX2	21q22.3	interferon-induced Mx protein
SMRT	U37146_at	U37146	PASS	9	26.56	PASS	13	9	11.23	2.36	2.36	SMRT		silencing mediator of retinoid and thyroid hormone action
DGK5Z	U51477_at	U51477	PASS	9	32.56	PASS	13	9	13.77	2.36	2.36	DGK2		diacylglycerol kinase, zeta (104kD)
LAMP1	J04182_at	J04182	PASS	9	47.78	PASS	13	9	20.23	2.36	2.36	LAMP1		lysosomal membrane glycoprotein-1
YWHAE	U54778 at	U54778	PASS	8	14.50	PASS	13	8	6.15	2.36	2.36			14-3-3 epsilon
U51333 s at	U51333 s at	U51333	PASS	9	47.11	PASS	13	9	20.00	2.36	2.36	HK3	5q35.2	hexokinase 3 (white cell)

CRFB4	Z17227_at	Z17227	PASS	9	15.78	PASS	10	9	6.70	2.35	2.35	IL10RB	21q22.1-q22.2	interleukin 10 receptor, beta	interleukin 10 receptor, beta
PIM2	U77735_at	U77735	PASS	6	24.33	PASS	12	6	10.33	2.35				pim-2 protooncogene homolog	similar to murine pim-2 product encoded by GenBank Accession Number L41495; serine/threonine protein kinase
AAMP	M95627_at	M95627	PASS	9	22.11	PASS	12	9	9.42	2.35	2.35	AAMP		angio-associated, migratory cell protein	angio-associated, migratory cell protein
K67 TOP2	D31891_at	D31891	PASS	9	18.56	PASS	11	9	7.91	2.35	2.35	KIAA0067		KIAA0067 gene product	KIAA0067 gene product
NKG2D	X54870_at	X54870	PASS	9	31.33	PASS	13	9	13.38	2.34	2.34	NKG2-D		Type II integral membrane protein	Type II integral membrane protein
M81695_s_a	M81695_s_a	M81695	PASS	9	32.22	PASS	13	9	13.77	2.34	2.34	ITGAX	16p13.1-p11	integrin, alpha X (antigen CD11C (p150), alpha polypeptide)	integrin, alpha X (antigen CD11C (p150), alpha polypeptide)
KRT12	U77643_at	U77643	PASS	8	28.25	PASS	13	8	12.08	2.34	2.34	SECTM1	17q25	secreted and transmembrane 1	secreted and transmembrane 1
LGALS9	AB006782_a	AB006782	PASS	9	78.89	PASS	13	9	33.77	2.34	2.34	LGALS9		lectin, galactoside-binding, soluble, 9 (galectin 9)	lectin, galactoside-binding, soluble, 9 (galectin 9)
ARF3	M74491_at	M74491	PASS	9	54.11	PASS	13	9	23.23	2.33	2.33	ARF3	12q13	ADP-ribosylation factor 3	ADP-ribosylation factor 3
ALDH7	U10868_at	U10868	PASS	8	16.88	PASS	12	8	7.25	2.33	2.33	ALDH7	11q13	aldehyde dehydrogenase 7	aldehyde dehydrogenase 7
M54915_s_a	M54915_s_a	M54915	PASS	9	54.67	PASS	13	9	23.54	2.32	2.32			pim-1 protein	pim-1 protein
FAH	M55150_at	M55150	PASS	6	18.50	PASS	8	6	8.00	2.31	2.31	FAH	15q23-q25	fumarylacetoacetate	fumarylacetoacetate
TPM3	HG3514-HT3	HG3514-H	PASS	9	149.22	PASS	13	9	64.54	2.31	2.31			focal adhesion kinase 2 (protein kinase B)	protein tyrosine kinase 2 beta
CAKB	U43522_at	U43522	PASS	8	14.13	PASS	9	8	6.11	2.31	2.31	PTK2B	8p21.1	intercellular adhesion molecule 3	intercellular adhesion molecule 3
ICAM3	X69819_at	X69819	PASS	9	52.22	PASS	13	9	22.62	2.31	2.31	ICAM3	19p13.3-p13.2	interferon regulatory factor 5	interferon regulatory factor 5
IRF5	U51127_at	U51127	PASS	9	29.00	PASS	7	9	12.57	2.31	2.31	IRF5	7q32	adenylyl cyclase-associated protein	putative
CAP	L12168_at	L12168	PASS	9	134.67	PASS	13	9	58.38	2.31	2.31	CAP		TATA box binding protein (TBP)-associated factor, RNA polymerase II, N, 68kD (RNA-binding protein 56)	TATA box binding protein (TBP)-associated factor, RNA polymerase II, N, 68kD (RNA-binding protein 56)
RBP56	U51334_at	U51334	PASS	8	25.50	PASS	13	8	11.08	2.30	2.30	TAF2N	17q11.1-q11.2	heat shock protein	70 kDa
HSPA1L	M11717_ma	M11717	PASS	9	53.11	PASS	13	9	23.08	2.30	2.30	HSPA1L		RaGDS-like	Protein sequence is in conflict with the conceptual translation.
RGL2	U68142_at	U68142	PASS	9	15.67	PASS	11	9	6.82	2.30	2.30	RGL2		pms5 protein	no similarities to reported gene products
PM5	X57398_at	X57398	PASS	9	27.33	PASS	12	9	11.92	2.29	2.29	pm5		capping protein (actin filament), gelsolin-like	capping protein (actin filament), gelsolin-like
K217	D86971_at	D86971	PASS	5	17.20	PASS	10	5	7.50	2.29	2.29	KIAA0217		Pin1	NIMA-interacting protein 1, essential mitotic regulator, essential peptidyl-prolyl isomerase
CAPG	M94345_at	M94345	PASS	9	49.33	PASS	13	9	21.54	2.29	2.29	CAPG	2cen-q24	interferon-induced leucine zipper protein	
PIN1	U49070_at	U49070	PASS	6	14.50	PASS	12	6	6.33	2.29	2.29	PIN1		integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide)	integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide)
U72882_s_at	U72882_s_at	U72882	PASS	6	15.50	PASS	9	6	6.78	2.29	2.29	IFP35		RasGAP-related protein	IQGAP2; Cdc42-, Rac1-, and calmodulin-binding protein
ITGAM	J03925_at	J03925	PASS	9	23.56	PASS	13	9	10.31	2.29	2.29	ITGAM	16p11.2		
IQGAP2	U51903_at	U51903	PASS	8	17.38	PASS	13	8	7.62	2.28	2.28	IQGAP2			

Z47038_s_at	Z47038_s_at	Z47038	PASS	8	12.88	PASS	11	8	5.91	2.18	2.18	2.18	putative microtubule associated protein 1A			open reading frame; N-terminal region
K224 DDX	D86977 at	D86977	PASS	8	15.25	PASS	13	8	7.00	2.18	2.18	2.18	KIAA0224			KIAA0224 gene product
K160	D63881 at	D63881	PASS	9	14.56	PASS	13	9	6.69	2.17	2.17	2.17	KIAA0160			KIAA0160 gene product is novel.
D83260_s_at	D83260_s_at	D83260	PASS	9	16.56	PASS	13	9	7.62	2.17	2.17	2.17	DXS9928E	Xq28	putative candidate disease gene XAP5	putative candidate disease gene XAP5
EIF3	U78525 at	U78525	PASS	9	19.56	PASS	13	9	9.00	2.17	2.17	2.17	EIF3S9		eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD)	eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD)
K169	D79991 at	D79991	PASS	9	13.67	PASS	10	9	6.30	2.17	2.17	2.17	KIAA0169		putative hydrophobic domain in amino acid positions 373-390.	putative hydrophobic domain in amino acid positions 373-390.
GZMA_ma1	M18737_ma	M18737	PASS	9	75.22	PASS	13	9	34.69	2.17	2.17	2.17	GZMA	5q11-q12	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)
PP1	U14603_at	U14603	PASS	9	76.56	PASS	13	9	35.31	2.17	2.17	2.17	PTP4A2	1p35	protein tyrosine phosphatase type IVA, member 2	protein tyrosine phosphatase type IVA, member 2
MLF2	U57342_at	U57342	PASS	9	26.00	PASS	13	9	12.00	2.17	2.17	2.17	MLF2		myelodysplasia/myeloid leukemia factor 2	
M84371_ma	M84371_ma	M84371	PASS	8	14.38	PASS	11	8	6.64	2.17	2.17	2.17	CD19			
H1X	D64142 at	D64142	PASS	9	54.89	PASS	13	9	25.38	2.16	2.16	2.16	H1FX		histone H1x	H1 histone family, member X
CMKBR2_ma	U95626_ma	U95626	PASS	8	36.75	PASS	13	8	17.00	2.16	2.16	2.16	ccr2		ccr2a	confirmed by similarity to Human monocyte chemoattractant protein 1 receptor (ccr2) alternatively spliced A-form, Encoded by GenBank Accession Number U80924, gi 1168965
U32986_s_at	U32986_s_at	U32986	PASS	9	24.67	PASS	12	9	11.42	2.16	2.16	2.16	DDB1	11q12-q13	damage-specific DNA binding protein 1 (127kD)	damage-specific DNA binding protein 1 (127kD)
MPP1	M64925_at	M64925	PASS	9	34.89	PASS	12	9	16.17	2.16	2.16	2.16	MPP1	Xq28	membrane protein, palmitoylated 1 (55kD)	membrane protein, palmitoylated 1 (55kD)
BCL2	M14745_at	M14745	PASS	9	16.22	PASS	13	9	7.54	2.15	2.15	2.15			bcl-2 protein	bcl-2 protein
DAGK1	X62535_at	X62535	PASS	9	38.56	PASS	13	9	17.92	2.15	2.15	2.15	DGKA	12	diacylglycerol kinase	diacylglycerol kinase, alpha (80kD)
M63438_s_at	M63438_s_at	M63438	PASS	9	167.11	PASS	13	9	77.77	2.15	2.15	2.15	TRADD			
TRADD	L41690_at	L41690	PASS	9	18.00	PASS	13	9	8.38	2.15	2.15	2.15			tumor necrosis factor receptor type 1 associated protein	TNFRSF1A-associated via death domain
PGM1	M83088 at	M83088	PASS	9	16.67	PASS	13	9	7.77	2.15	2.15	2.15	PGM1	1p22.1	phosphoglucomutase 1	phosphoglucomutase 1
CRIP1	U09770 at	U09770	PASS	9	35.33	PASS	12	9	16.50	2.14	2.14	2.14	hCRHP		cysteine-rich heart protein	
K43 HOM	D26362 at	D26362	PASS	8	17.13	PASS	9	8	8.00	2.14	2.14	2.14	KIAA0043			KIAA0043 gene product
MYD88	U70451_at	U70451	PASS	8	38.13	PASS	13	8	17.85	2.14	2.14	2.14	MYD88	3p22	myeloid differentiation primary response gene (88)	myeloid differentiation primary response gene (88)
HNRPH1	L22009_at	L22009	PASS	9	74.00	PASS	13	9	34.69	2.13	2.13	2.13			hnRNP H	49 kDa protein; heterogeneous nuclear ribonucleoprotein H
MX11	L07648 at	L07648	PASS	9	17.56	PASS	13	9	8.23	2.13	2.13	2.13	MX11			
GUK1	L76200 at	L76200	PASS	8	56.25	PASS	13	8	26.38	2.13	2.13	2.13	GUK1	1q32-q42	guanylate kinase 1	guanylate kinase 1
C8FWPH	AJ000480 at	AJ000480	PASS	5	11.60	PASS	9	5	5.44	2.13	2.13	2.13	C8FW		phosphoprotein	
GNG11	U31384_at	U31384	PASS	9	38.78	PASS	13	9	18.23	2.13	2.13	2.13	GNG11		guanine nucleotide binding protein 11	guanine nucleotide binding protein 11
HG3076-HT	HG3076-HT	HG3076-H	PASS	9	52.33	PASS	13	9	24.62	2.13	2.13	2.13				
UGT2B4	U03105 at	U03105	PASS	7	19.86	PASS	11	7	9.36	2.12	2.12	2.12			B4-2 protein	

DPYSL2	U97105_at	U97105	PASS	8	18.75	PASS	13	8	8.85	2.12	2.12	DPYSL2	8p22-p21	dihydropyrimidinase-like 2
GGTB2	D29805_at	D29805	PASS	9	40.89	PASS	13	9	19.31	2.12	2.12	B4GALT1	9p13	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1
M61827_ma	M61827_ma	M61827	PASS	9	33.22	PASS	10	9	15.70	2.12	2.12	SPN		leukosialin
D63479_s_at	D63479_s_at	D63479	PASS	9	18.67	PASS	12	9	8.83	2.11	2.11	DGKD		diacylglycerol kinase, delta (130kD)
IP	L47738_at	L47738	PASS	9	29.22	PASS	12	9	13.83	2.11	2.11			inducible protein
X98534_s_at	X98534_s_at	X98534	PASS	8	25.50	PASS	13	8	12.08	2.11	2.11	VASP	19q13.2-q13.3	vasodilator-stimulated phosphoprotein
CALM1	HG1862-HT	HG1862-H	PASS	9	91.11	PASS	13	9	43.15	2.11	2.11			
HPK1	U66464_at	U66464	PASS	9	16.89	PASS	13	9	8.00	2.11	2.11	HPK1		hematopoietic progenitor
FKBP2	M75099_at	M75099	PASS	9	23.56	PASS	12	9	11.17	2.11	2.11	FKBP2	11q13.1-q13.3	FK506-binding protein 2 (13kD)
CMKBR7	L31584_at	L31584	PASS	9	39.89	PASS	13	9	18.92	2.11	2.11	CCR7	17q12-q21.2	chemokine (C-C motif) receptor 7
GPRK6	L16862_at	L16862	PASS	7	25.29	PASS	7	7	12.00	2.11	2.11	GPRK6	5q35	G protein-coupled receptor kinase 6
FCER1G	M33195_at	M33195	PASS	9	112.00	PASS	13	9	53.15	2.11	2.11	FCER1G	1q23	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
MRP	HG1612-HT	HG1612-H	PASS	8	20.00	PASS	12	8	9.50	2.11	2.11			
LYL1	M22638_at	M22638	PASS	8	14.38	PASS	12	8	6.83	2.10	2.10	LYL1		
IRAK1	L76191_at	L76191	PASS	9	32.67	PASS	13	9	15.54	2.10	2.10	IRAK1	Xq28	interleukin-1 receptor-associated kinase 1
PI4KB	U81802_at	U81802	PASS	7	14.71	PASS	11	7	7.00	2.10	2.10	PIK4CB	1q21	phosphatidylinositol 4-kinase, catalytic, beta polypeptide
GT335	U53003_at	U53003	PASS	9	12.22	PASS	11	9	5.82	2.10	2.10	GT335		similar to E. coli SCR27A and to zebrafish ESI
M58286_s_a	M58286_s_at	M58286	PASS	7	17.43	PASS	10	7	8.30	2.10	2.10	TNFRSF1A	12p13.2	tumor necrosis factor receptor 1 (55kD)
PSMA28	D45248_at	D45248	PASS	9	69.44	PASS	13	9	33.08	2.10	2.10	PSME2	14q11.2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
CKAP1	D49738_at	D49738	PASS	9	34.56	PASS	13	9	16.46	2.10	2.10	CKAP1	19q13.11-q13.12	cytoskeleton-associated protein 1
HG4334-HT4	HG4334-HT4	HG4334-H	PASS	6	14.50	PASS	12	6	6.92	2.10	2.10			
SRF	J03161_at	J03161	PASS	6	18.83	PASS	9	6	9.00	2.09	2.09	SRF		serum response factor (c-fos serum response element-binding transcription factor)
CRAA	U78556_at	U78556	PASS	8	15.75	PASS	13	8	7.54	2.09	2.09	hCRA alpha		cisplatin resistance associated alpha protein
S83513_s_at	S83513_s_at	S83513	PASS	7	11.14	PASS	9	7	5.33	2.09	2.09	ADCYAP1	18p11	adenylate cyclase activating polypeptide 1 (pituitary)
VCL	M33308_at	M33308	PASS	9	50.22	PASS	13	9	24.08	2.09	2.09	VCL	10q11.2-qter	vinculin
K183	D80005_at	D80005	PASS	9	25.00	PASS	13	9	12.00	2.08	2.08	KIAA0183		
J04046_s_at	J04046_s_at	J04046	PASS	8	29.13	PASS	12	8	14.00	2.08	2.08	CALM1		calmodulin
STXBP3	D63851_at	D63851	PASS	5	9.80	PASS	7	5	4.71	2.08	2.08	STXBPI	9q34.1	syntaxin binding protein 1
COPA	U24105_at	U24105	PASS	9	36.78	PASS	13	9	17.69	2.08	2.08	COPA		coatomer protein complex, subunit alpha
DDB2	U18300_at	U18300	PASS	9	12.11	PASS	12	9	5.83	2.08	2.08	DDB2	11p12-p11	damage-specific DNA binding protein 2 (48kD)
MLN_ma1	X15393_ma1	X15393	PASS	7	13.29	PASS	10	7	6.40	2.08	2.08	motilin		motilin

ETR3	U69546_at	U69546	PASS	7	22.71	PASS	13	7	11.15	2.04	2.04			ETR-3	protein contains 3 RRM motifs that may bind RNA; putative RNA binding protein; Elav-type ribonucleoprotein; complete sequence of human EST, GenBank Accession Number R57293
GSK3A	L40027_at	L40027	PASS	9	19.89	PASS	13	9	9.77	2.04	2.04			glycogen synthase kinase 3	exon 1 part (leader region): bp6-77; exon 2 part (alpha-1 domain): bp78-347; exon 3 part (alpha-2 domain): bp348-623; exon 4 part (alpha-3 domain): bp624-899; exon 5 part (transmembrane region): bp900-1016; exon 6 part (cytoplasmic region): bp1017-1049; exon 7 part (cytoplasmic region): bp1050-1097; exon 8 part (cytoplasmic region): bp1098-1103
HLA-A_f	D32129_f_at	D32129	PASS	9	342.11	PASS	13	9	168.23	2.03	2.03			HLA-A26	
RB1	L22343_at	L22343	PASS	7	12.86	PASS	9	7	6.33	2.03	2.03			nuclear phosphoprotein	IFN-induced
PIK4	L36151_at	L36151	PASS	9	39.89	PASS	13	9	19.69	2.03	2.03		PIK4CA	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	
SPS2	U43286_at	U43286	PASS	9	13.67	PASS	12	9	6.75	2.02	2.02		SPS2	selenophosphate synthetase 2	the amino acid residue number 60 is a selenocysteine encoded by the TGA (UGA) codon; We designated this enzyme selenophosphate synthetase 2 to distinguish it from the human homolog described by Low, S.C., Hamey, J.W. and Berry, M.J. J. Biol. Chem. 270, 21659-21664 (1995) (GenBank Accession Number U34044)
HYP4	U81556_at	U81556	PASS	9	40.44	PASS	13	9	20.00	2.02	2.02			hypothetical protein A4	
3PK	U09578_at	U09578	PASS	8	17.25	PASS	13	8	8.54	2.02	2.02		MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	
K23_CAN	D14689_at	D14689	PASS	9	32.11	PASS	12	9	15.92	2.02	2.02		KIAA0023		KIAA0023 gene product
RNA_OSTB	AB000115_a	AB000115	PASS	7	12.86	PASS	8	7	6.38	2.02	2.02				The submitters designated this product as GS3686
IL2RG	D11086_at	D11086	PASS	9	42.00	PASS	13	9	20.85	2.01	2.01		IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency)	interleukin 2 receptor, gamma (severe combined immunodeficiency)
SEC14L	D67029_at	D67029	PASS	5	15.60	PASS	12	5	7.75	2.01	2.01		SEC14L	SEC14 (S. cerevisiae)-like	SEC14 (S. cerevisiae)-like
POLG	U60325_at	U60325	PASS	6	13.33	PASS	8	6	6.63	2.01	2.01		POLG	polymenase (DNA directed), gamma	polymenase (DNA directed), gamma
K142_K6	D63476_at	D63476	PASS	9	14.22	PASS	13	9	7.08	2.01	2.01		P85SPR	PAK-interacting exchange factor beta	PAK-interacting exchange factor beta
FCGR1A	M63835_at	M63835	PASS	7	12.29	PASS	8	7	6.13	2.01	2.01		FCGR1A	IgG Fc receptor 1	Fc fragment of IgG, high affinity Ia receptor for (CD64)
MLK3	L32976_at	L32976	PASS	7	12.29	PASS	7	7	6.14	2.00	2.00		MLK3	mixed lineage kinase 3	mixed lineage kinase 3
E_CCA12	U06681_at	U06681	PASS	5	12.40	PASS	10	5	6.20	2.00	2.00				

FACLI	D10040_at	D10040	PASS	5	12.00	PASS	9	5	6.00	2.00	2.00	FACLI	3q13	fatty-acid-Coenzyme A ligase, long-chain 1	fatty-acid-Coenzyme A ligase, chain 1
MCM6	D84557_at	D84557	PASS	9	13.44	PASS	11	9	6.73	2.00	2.00			HsMcm6	
BRCA2	U50523_at	U50523	PASS	9	84.89	PASS	13	9	42.54	2.00	2.00				
BIOC3	AFEX-BioC-AFFX-BioC		fail	4		PASS	13	4	14.46	Normal	Normal				
L15189_s_at	L15189_s_at	L15189	fail	4		PASS	13	4	6.77	Normal	Normal	HSPA9B	5q31.1	heat shock 70kD protein 9B (mortalin-2)	heat shock 70kD protein 9B (mortalin-2)
NIP71	U83843_at	U83843	fail	4		PASS	13	4	6.77	Normal	Normal	Nip7-1		HIV-1 Nef interacting protein	similar to murine CCT (chaperonin containing TCP-1) eta subunit encoded by GenBank Accession Number Z31399; CCT assists the folding of proteins in eukaryotic cytosol; Nef enhances the infectivity of HIV and SIV
APT1	D49396_at	D49396	fail	4		PASS	13	4	4.85	Normal	Normal			Aop1_Human, MER5(Aop1_Mouse)-like protein	
RAB1	M28209_at	M28209	fail	3		PASS	13	3	6.23	Normal	Normal	RAB1	2p14-p13.4	RAB1, member RAS oncogene family	RAB1, member RAS oncogene family
M28213_s_at	M28213_s_at	M28213	fail	3		PASS	13	3	5.77	Normal	Normal	RAB2		RAB2, member RAS oncogene family	RAB2, member RAS oncogene family
L00634_s_at	L00634_s_at	L00634	fail	2		PASS	13	2	6.15	Normal	Normal	FNTA	8p22-q11	farnesyltransferase, CAAX box, alpha	farnesyltransferase, CAAX box, alpha
PEPD	J04605_at	J04605	fail	2		PASS	13	2	5.38	Normal	Normal	PEPD	19q12-q13.2	peptidase D	peptidase D
SEC7PL	U59752_at	U59752	fail	4		PASS	12	4	7.92	Normal	Normal	PSCD2		pleckstrin homology, Sec7 and coiled/coil domains 2 (cytohesin-2)	pleckstrin homology, Sec7 and coiled/coil domains 2 (cytohesin-2)
KI12	D25218_at	D25218	fail	4		PASS	12	4	6.42	Normal	Normal	KIAA0112		transcription elongation factor A (SII)-like 1	transcription elongation factor A (SII)-like 1
PP21	M99701_at	M99701	fail	4		PASS	12	4	5.75	Normal	Normal	TCEAL1	Xq22.1		
AFEX-BioB-AFFX-BioB	U89355_at	U89355	fail	3		PASS	12	3	10.75	Normal	Normal	CREBBP	16p13.3	CREB binding protein (Rubinstein-Taybi syndrome)	CREB binding protein (Rubinstein-Taybi syndrome)
E_CREBBP	U89355_at	U89355	fail	3		PASS	12	3	5.17	Normal	Normal			culin 1	culin 1
CUL1	U58087_at	U58087	fail	4		PASS	11	4	8.64	Normal	Normal	CUL1		long-chain acyl-CoA synthetase	ATP-binding domain (bp. 1447..1846)
L09229_s_at	L09229_s_at	L09229	fail	4		PASS	11	4	8.36	Normal	Normal	FACLI		mitochondrial citrate transport protein	
SLC20A3_m	X96924_m	X96924	fail	4		PASS	11	4	8.18	Normal	Normal				
K233_COST	D87071_at	D87071	fail	4		PASS	11	4	7.45	Normal	Normal	KIAA0233		KIAA0233 gene product	
E_23773	U90904_at	U90904	fail	4		PASS	11	4	7.00	Normal	Normal				
MTHFD	L38928_at	L38928	fail	4		PASS	11	4	6.73	Normal	Normal			5,10-methylenetetrahydrofolate synthetase	
MEF	U32645_at	U32645	fail	4		PASS	11	4	6.27	Normal	Normal	ELF4		E74-like factor 4 (ets domain transcription factor)	E74-like factor 4 (ets domain transcription factor)
OAT	M29927_at	M29927	fail	4		PASS	11	4	6.00	Normal	Normal	OAT	10q26	ornithine aminotransferase (gyrate atrophy)	ornithine aminotransferase (gyrate atrophy)
MPV17	X76538_at	X76538	fail	4		PASS	11	4	5.82	Normal	Normal	MPV17	2p23-p21	MpV17 transgene, murine homolog, glomerulosclerosis	MpV17 transgene, murine homolog, glomerulosclerosis
FH	U59309_at	U59309	fail	4		PASS	11	4	5.73	Normal	Normal	FH	1q42.1	fumarate hydratase	fumarate hydratase
GBP1	M55542_at	M55542	fail	4		PASS	11	4	5.64	Normal	Normal	GBP1	1	guanylate binding protein 1, interferon-inducible, 67kD	guanylate binding protein 1, interferon-inducible, 67kD
ARF6	M57763_at	M57763	fail	3		PASS	11	3	7.64	Normal	Normal	ARF6		ADP-ribosylation factor 6	ADP-ribosylation factor 6

GUBP	U78524_at	U78524	fail	3	PASS	11	3	6.00	Normal	Normal	DDXBP1	15q	DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1	DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1
E 23828	U79285 at	U79285	fail	3	PASS	11	3	5.73	Normal	Normal				
PTEN	U92436 at	U92436	fail	3	PASS	11	3	5.00	Normal	Normal	PTEN	10q23	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
SLBP	U75679 at	U75679	fail	3	PASS	11	3	4.91	Normal	Normal	SLBP		histone stem-loop binding protein	
AFFX-HSAC	AFFX-HSAC	AFFX-HSA	fail	1	PASS	11	1	7.27	Normal	Normal				
U04806 s at	U04806 s at	U04806	fail	4	PASS	10	4	8.90	Normal	Normal			FLT3/FLK2 ligand	
TRIP7	L40357 at	L40357	fail	4	PASS	10	4	7.60	Normal	Normal	TRIP7		thyroid receptor interactor 7	thyroid hormone receptor interactor 7
STAT1	M97936 at	M97936	fail	4	PASS	10	4	7.50	Normal	Normal				
LRMP	U10485 at	U10485	fail	4	PASS	10	4	7.00	Normal	Normal	LRMP		lymphoid-restricted membrane protein	lymphoid-restricted membrane protein
LAP18 ma	M31303 ma	M31303	fail	4	PASS	10	4	6.60	Normal	Normal	Op18		oncoprotein 18	
DIFF48	U49187 at	U49187	fail	4	PASS	10	4	6.50	Normal	Normal	Diff48			
SNRPD3	U15009 at	U15009	fail	4	PASS	10	4	6.40	Normal	Normal	SNRPD3		small nuclear ribonucleoprotein D3 polypeptide (18kD)	small nuclear ribonucleoprotein D3 polypeptide (18kD)
XG2153 s at	XG2153 s at	XG2153	fail	4	PASS	10	4	6.30	Normal	Normal			PI 1h protein	
CTR2	U83461 at	U83461	fail	4	PASS	10	4	6.20	Normal	Normal	SLC31A2	9q31-q32	solute carrier family 31 (copper transporters), member 2	solute carrier family 31 (copper transporters), member 2
GPCR	L42324 at	L42324	fail	4	PASS	10	4	6.10	Normal	Normal	GPCR		G protein-linked receptor	
EIF5	U49436 at	U49436	fail	4	PASS	10	4	6.00	Normal	Normal	EIF5		eukaryotic translation initiation factor 5	eukaryotic translation initiation factor 5
K100 EL	D43947 at	D43947	fail	4	PASS	10	4	5.90	Normal	Normal	KIAA0100		KIAA0100 gene product	KIAA0100 gene product
K274 HYON	D87464 at	D87464	fail	4	PASS	10	4	5.90	Normal	Normal	KIAA0274		KIAA0274 gene product	KIAA0274 gene product
GOT2	M22632 at	M22632	fail	4	PASS	10	4	5.90	Normal	Normal	GOT2	16q21	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
DGUOK	U41668 at	U41668	fail	4	PASS	10	4	5.90	Normal	Normal	DGUOK		deoxyguanosine kinase	deoxyguanosine kinase
IRRCP	U18321 at	U18321	fail	4	PASS	10	4	5.80	Normal	Normal	DAP3	1q21	Death associated protein 3	Death associated protein 3
HZF1	X78924 at	X78924	fail	4	PASS	10	4	5.80	Normal	Normal	HZF1		zinc finger protein	
D29640 s at	D29640 s at	D29640	fail	4	PASS	10	4	5.70	Normal	Normal	SAR1	15	rasGAP-like with IQ motifs	rasGAP-like with IQ motifs
SNRPA1	X13482 at	X13482	fail	4	PASS	10	4	5.60	Normal	Normal	SNRPA1		small nuclear ribonucleoprotein polypeptide A'	small nuclear ribonucleoprotein polypeptide A'
U47686 s at	U47686 s at	U47686	fail	4	PASS	10	4	5.10	Normal	Normal			signal transducer and activator of transcription Stat5B	STAT protein; is activated by IL-2, IL-7, IL-15, growth hormone, IL-3, GM-CSF, thrombopoietin, prolactin, and erythropoietin; tyrosine 699 phosphorylation is required for activation and dimerization of Stat5B
K267_NAHE	D87743 at	D87743	fail	4	PASS	10	4	4.80	Normal	Normal	KIAA0267		Similar to Human Na+/H+ exchanger 2 (A57644)	Similar to Human Na+/H+ exchanger 2 (A57644)
RPP38	U77664 at	U77664	fail	4	PASS	10	4	4.70	Normal	Normal	RPP38		RNaseP protein P38	RNaseP protein P38
L38593 s at	L38593 s at	L38593	fail	3	PASS	10	3	6.50	Normal	Normal	NRAMP1		integral membrane protein	alternative
TBI	M74089 at	M74089	fail	3	PASS	10	3	5.50	Normal	Normal	TBI			
CHED	M80629 at	M80629	fail	3	PASS	10	3	5.30	Normal	Normal	CDC2L		cholinesterase-related cell division controller	cholinesterase-related cell division controller
RCPN	U03644 at	U03644	fail	3	PASS	10	3	5.30	Normal	Normal	CIR		CBF1 interacting corepressor	CBF1 interacting corepressor
CCNG2	U47414 at	U47414	fail	3	PASS	10	3	5.30	Normal	Normal	CCNG2		cyclin G2	cyclin G2
E 23721	U79291 at	U79291	fail	3	PASS	10	3	5.00	Normal	Normal				

LIVP	L13800 at	L13800	fail	3		PASS	10	3	4.90	Normal	Normal	PXMP3	8q21.1	peroxisomal membrane protein 3 (35kD, Zellweger syndrome)
PXMP3	M86852_at	M86852	fail	3		PASS	10	3	4.80	Normal	Normal			peroxisomal membrane protein 3 (35kD, Zellweger syndrome)
CPSPF	U37012_at	U37012	fail	4		PASS	9	4	8.00	Normal	Normal			cleavage and polyadenylation specificity factor
CD9	M38690 at	M38690	fail	4		PASS	9	4	7.33	Normal	Normal	CD9	12p13	CD9 antigen (p24)
CASM	AF000177_at	AF000177	fail	4		PASS	9	4	7.11	Normal	Normal	CaSm		CaSm
														motifs; overexpressed in pancreatic cancer
K138_THH	D50928 at	D50928	fail	4		PASS	9	4	7.00	Normal	Normal	K1AA0138		K1AA0138 gene product
PHBLN1	U03891_at	U03891	fail	4		PASS	9	4	5.89	Normal	Normal	DJ742C19.2	22q12.3-q13.1	phorbol (similar to apolipoprotein B mRNA editing protein)
HLA-DPB1	M83664 at	M83664	fail	4		PASS	9	4	5.67	Normal	Normal	HLA-DPB1		HLA-DPB1
K251_COSC	D87438 at	D87438	fail	4		PASS	9	4	5.44	Normal	Normal	K1AA0251		Similar to a C.elegans protein in cosmid C14H10
SORD	L29008 at	L29008	fail	4		PASS	9	4	5.33	Normal	Normal	SORD	15q15-q21.1	sorbitol dehydrogenase
K92_MYH6	D42054 at	D42054	fail	4		PASS	9	4	5.22	Normal	Normal	K1AA0092		K1AA0092 gene product
RECA	L07493 at	L07493	fail	4		PASS	9	4	4.89	Normal	Normal	RPA3	7	replication protein A3 (14kD)
SCP2	U11313 at	U11313	fail	4		PASS	9	4	4.89	Normal	Normal	SCP2	1pter-p21	sterol carrier protein 2
YAF2	U72209 at	U72209	fail	4		PASS	9	4	4.78	Normal	Normal	YAF2		sterol carrier protein 2
PPP2R1B	M65254_at	M65254	fail	4		PASS	9	4	4.56	Normal	Normal	PPP2R1B	11q23	YY1-associated factor 2 (formerly protein phosphatase 2A)
														regulatory subunit A (PR 65), beta isoform
CD94	U30610_at	U30610	fail	3		PASS	9	3	8.44	Normal	Normal	KLRD1	12p13	killer cell lectin-like receptor subfamily D, member 1
SNRNP2	M15841_at	M15841	fail	3		PASS	9	3	7.44	Normal	Normal	SNRNP2		small nuclear ribonucleoprotein polypeptide B*
CLC	L01664 at	L01664	fail	3		PASS	9	3	7.22	Normal	Normal	CLC	19q13.1	Charot-Leyden crystal protein
AFEX-HUM	AFEX-HUM	AFEX-HUM	fail	3		PASS	9	3	7.11	Normal	Normal			
SNX1	U53225 at	U53225	fail	3		PASS	9	3	6.67	Normal	Normal	SNX1		sorting nexin 1
FKBP5	U42031 at	U42031	fail	3		PASS	9	3	6.56	Normal	Normal	FKBP5		FK506-binding protein 5
S72024 s at	S72024 s at	S72024	fail	3		PASS	9	3	6.44	Normal	Normal	cif-5A		eukaryotic initiation factor 5A
SMARCC1	U66615_at	U66615	fail	3		PASS	9	3	5.67	Normal	Normal	SMARCC1	3p23-p21	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
L05624 s at	L05624 s at	L05624	fail	3		PASS	9	3	5.56	Normal	Normal			
TPP2	M73047 at	M73047	fail	3		PASS	9	3	5.56	Normal	Normal	TPP2	13q32-q33	tripeptidyl peptidase II
PLK	U01038 at	U01038	fail	3		PASS	9	3	5.56	Normal	Normal			
STAT6	U16031_at	U16031	fail	3		PASS	9	3	5.56	Normal	Normal	STAT6	12q13	pLK
														signal transducer and activator of transcription 6, interleukin-4 induced
NUP88	Y08612 at	Y08612	fail	3		PASS	9	3	5.44	Normal	Normal	NUP88	17p13	nucleoporin 88kD
S79219 s at	S79219 s at	S79219	fail	3		PASS	9	3	5.22	Normal	Normal	PCCA	13q32	propionyl Coenzyme A carboxylase, alpha polypeptide

C2f	U72514_at	U72514	fail	3	PASS	9	3	5.00	Normal	Normal	C2f	C2f	similar to EST with GenBank Accession Number R64505; similar to S. cerevisiae hypothetical protein L9470.5 encoded by GenBank Accession Number S51431, and to S. pombe hypothetical 34.9 KD protein encoded by GenBank Accession Number Z68198; see corresponding genomic sequence in GenBank Accession Number U72506
E 23733	U72514_at	U72514	fail	3	PASS	9	3	5.00	Normal	Normal			
DCK	M60527_at	M60527	fail	3	PASS	9	3	4.67	Normal	Normal	DCK	4q13.3-q21.1	deoxycytidine kinase
AFEX-BioB	AFEX-BioB	AFEX-BioB	fail	0	PASS	9	0	17.44	Normal	Normal			
RES424A	AB000464_at	AB000464	fail	4	PASS	8	4	8.50	Normal	Normal			
SSRP1	M86737_at	M86737	fail	4	PASS	8	4	7.75	Normal	Normal	SSRP1	11q12	structure specific recognition protein 1
BAT3	M33521_at	M33521	fail	4	PASS	8	4	7.50	Normal	Normal	D6S52E	6p21.3	HLA-B associated transcript-3
PNOC	U48263_at	U48263	fail	4	PASS	8	4	7.00	Normal	Normal	OFQ		pre-pro-orphanin FQ
ERCCI	M13194_at	M13194	fail	4	PASS	8	4	6.63	Normal	Normal	ERCCI	19q13.2-q13.3	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)
TRNAGUTR	U30888_at	U30888	fail	4	PASS	8	4	6.38	Normal	Normal	USP14		tRNA-Guanine Transglycosylase
L24774_s_at	L24774_s_at	L24774	fail	4	PASS	8	4	5.88	Normal	Normal	DCI	16p13.3	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
HG3319-HT3	HG3319-HT3	HG3319-HT3	fail	4	PASS	8	4	5.63	Normal	Normal			
G9	X78687_at	X78687	fail	4	PASS	8	4	5.38	Normal	Normal	NEU	6 or 10pter-q23	neuraminidase
ZNF139	U09848_at	U09848	fail	4	PASS	8	4	5.00	Normal	Normal	ZNF139		zinc finger protein 139 (clone pHZ-37)
ZFX	X59739_at	X59739	fail	4	PASS	8	4	5.00	Normal	Normal	ZFX	Xp22.1-p21.3	zinc finger protein, X-linked
S80267_s_at	S80267_s_at	S80267	fail	4	PASS	8	4	4.88	Normal	Normal	p72syk		This sequence comes from Fig. 3.
DARS	J05032_at	J05032	fail	4	PASS	8	4	4.63	Normal	Normal	DARS		aspartyl-tRNA synthetase
U18271 cds	U18271 cds	U18271	fail	4	PASS	8	4	4.63	Normal	Normal	TMPO		thymopoietin beta
K128_HCDC	D50918_at	D50918	fail	3	PASS	8	3	7.13	Normal	Normal	K1AA0128		The K1AA0128 gene is related to cdc10.
TDRAA	HG3578-HT3	HG3578-HT3	fail	3	PASS	8	3	6.25	Normal	Normal			
LAMB2	M94362_at	M94362	fail	3	PASS	8	3	6.00	Normal	Normal	LAMB2		lamin B2
SH3BP2	U32519_at	U32519	fail	3	PASS	8	3	5.50	Normal	Normal			GAP SH3 binding protein
MURR1	D85433_at	D85433	fail	3	PASS	8	3	5.38	Normal	Normal			
ITGAE	L25851_at	L25851	fail	3	PASS	8	3	5.25	Normal	Normal	ITGAE		integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)
SPLREGSUP	U08377_at	U08377	fail	3	PASS	8	3	5.25	Normal	Normal	SFRS8		splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot, Drosophila homolog)

Table 1. Summary of the results of the analysis of the 1000 Genomes Project data for the 1000 Genomes Project data.

K03498_xptl	K03498_xptl	K03498	fail	4	PASS	7	4	5.57	Normal	Normal		pol. protein	env ORF (bases 110-290) first start codon at 191.; putative
SL1	L39059_at	L39059	fail	4	PASS	7	4	5.43	Normal	Normal		transcription factor SL1	
PIGF	D13435_at	D13435	fail	4	PASS	7	4	5.29	Normal	Normal	PIGF	2p21-p16	phosphatidylinositol glycan, class F
TCF4	M74719_at	M74719	fail	4	PASS	7	4	5.14	Normal	Normal	TCF4	18q21.1	transcription factor 4
GOLGA1	U51587_at	U51587	fail	4	PASS	7	4	5.14	Normal	Normal	GOLGA1		golgi autoantigen, golgm subfamily 2, 1
X75091_s_at	X75091_s_at	X75091	fail	4	PASS	7	4	5.00	Normal	Normal			PHAPII (Putative HLA DR Associated Protein II)
POLR3	U93867_at	U93867	fail	4	PASS	7	4	4.71	Normal	Normal	RPC62		RNA polymerase III subunit
GLCLC	M90656_at	M90656	fail	4	PASS	7	4	4.43	Normal	Normal	GLCLC	6p12	glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD)
PTPRE	HGG20-HT63	HGG20-HT	fail	3	PASS	7	3	8.00	Normal	Normal			
OBRGRP	Y12670_at	Y12670	fail	3	PASS	7	3	8.00	Normal	Normal	OB-RGRP		leptin receptor gene-related protein
DRNM23	U29656_at	U29656	fail	3	PASS	7	3	7.29	Normal	Normal	NME3	16q13	non-metastatic cells 3, protein expressed in
OMD	AB000114_at	AB000114	fail	3	PASS	7	3	6.86	Normal	Normal	OMD		osteomodulin
RY1	X76302_at	X76302	fail	3	PASS	7	3	6.86	Normal	Normal	RY-1		nucleic acid binding protein
K12_TOLL	D13637_at	D13637	fail	3	PASS	7	3	6.57	Normal	Normal	TLR1	4p14	toll-like receptor 1
CSNK2A1	M55265_at	M55265	fail	3	PASS	7	3	5.86	Normal	Normal	CSNK2A1	20p13	casein kinase 2, alpha 1 polypeptide
DOC2	U53446_at	U53446	fail	3	PASS	7	3	5.86	Normal	Normal	DAB2	5p13	disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)
SMARCD1	U66617_at	U66617	fail	3	PASS	7	3	5.71	Normal	Normal	SMARCD1	12q13-q14	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1
ZNF131	U09410_at	U09410	fail	3	PASS	7	3	5.43	Normal	Normal	ZNF131		zinc finger protein 131 (clone pHZ-10)
GLIPR	U16307_at	U16307	fail	3	PASS	7	3	5.43	Normal	Normal	GLIPR		glioma pathogenesis-related protein
E2F5	U31556_at	U31556	fail	3	PASS	7	3	5.43	Normal	Normal	E2F-5		transcription factor
BARD1	U76638_at	U76638	fail	3	PASS	7	3	4.29	Normal	Normal	BARD1	2q34-q35	BRCA1 associated RING domain 1
U40763_s_at	U40763_s_at	U40763	fail	3	PASS	7	3	4.14	Normal	Normal	CYP		Clk-associating RS-cyclophilin
ARH9	L25081_at	L25081	fail	2	PASS	7	2	8.86	Normal	Normal	ARHC	1p21-p13	ras homolog gene family, member C
HSN	U03057_at	U03057	fail	2	PASS	7	2	8.86	Normal	Normal	SNL	7p22	singed (Drosophila)-like (sea urchin fascin homolog like)
TARS	M63180_at	M63180	fail	2	PASS	7	2	5.57	Normal	Normal	TARS	5p13-ccn	threonyl-tRNA synthetase
K182	D80004_at	D80004	fail	2	PASS	7	2	5.43	Normal	Normal	KIAA0182		
TFAP3B	U91931_at	U91931	fail	2	PASS	7	2	5.43	Normal	Normal	ADTB3		Beta-3A-adaptin
CTIP	U72066_at	U72066	fail	2	PASS	7	2	5.14	Normal	Normal	RBBP8	18q11.2	retinoblastoma-binding protein 8
CD72	M54992_at	M54992	fail	2	PASS	7	2	5.00	Normal	Normal	CD72	9p	CD72 antigen
PDE6B	S41458_at	S41458	fail	2	PASS	7	2	4.86	Normal	Normal	PDE6B	4p16.3	phosphodiesterase 6B, cGMP-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant)

GTBP	U73737_at	U73737	fail	2		PASS	7	2	4.86	Normal	Normal	GTBP	2p16	G/T mismatch-binding protein	G/T mismatch-binding protein
U67932_s at	U67932_s at	U67932	fail	2		PASS	7	2	4.57	Normal	Normal	Pdc7A2		cAMP phosphodiesterase	
GBE1	L07956_at	L07956	fail	2		PASS	7	2	4.43	Normal	Normal	GBE1	3p21	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)
CDR2	M63256_at	M63256	fail	2		PASS	7	2	4.43	Normal	Normal	CDR2	16p13.1-p12	major Yo paraneoplastic antigen	cerebellar degeneration-related protein (62kD)
RP1H	U90437_at	U90437	fail	2		PASS	7	2	4.29	Normal	Normal				
HNRPA0	U23803_at	U23803	fail	1		PASS	7	1	8.71	Normal	Normal			heterogeneous ribonucleoprotein A0	hnRNP protein; hnRNA binding protein
ICRF	Z69915_at	Z69915	fail	1		PASS	7	1	6.00	Normal	Normal				
SSR1	Z12830_at	Z12830	fail	1		PASS	7	1	5.86	Normal	Normal	SSR1		signal sequence receptor, alpha (translocon-associated protein alpha)	signal sequence receptor, alpha (translocon-associated protein alpha)
RALGDS	U14417_at	U14417	fail	1		PASS	7	1	5.71	Normal	Normal			Ral guanine nucleotide dissociation stimulator	the C-terminal non-catalytic domain of the Ral GDS interacts with Ras
SMARCC2	U66616_at	U66616	fail	1		PASS	7	1	5.71	Normal	Normal	SMARCC2	12q13-q14	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2
PCCB	S67325_at	S67325	fail	1		PASS	7	1	5.29	Normal	Normal	PCCB	3q21-q22	propionyl Coenzyme A carboxylase, beta polypeptide	propionyl Coenzyme A carboxylase, beta polypeptide
G16P	U50839_at	U50839	fail	1		PASS	7	1	5.00	Normal	Normal	g16		g16 protein	
CUL2	U83410_at	U83410	fail	1		PASS	7	1	5.00	Normal	Normal	CUL2		cullin 2	cullin 2
CEBPG	U20240_at	U20240	fail	1		PASS	7	1	4.86	Normal	Normal	CEBPG		CCAAT/enhancer binding protein (C/EBP), gamma	CCAAT/enhancer binding protein (C/EBP), gamma
RAB9	U44103_at	U44103	fail	1		PASS	7	1	4.86	Normal	Normal	RAB9		RAB9, member RAS oncogene family	RAB9, member RAS oncogene family
K55 TRE	D29956_at	D29956	fail	1		PASS	7	1	4.43	Normal	Normal	USP8		ubiquitin specific protease 8	ubiquitin specific protease 8
CRIP2	D42123_at	D42123	PASS	9	25.56	fail	5	9		Disease	Disease	CRIP2	14q32.3	cysteine-rich protein 2	cysteine-rich protein 2
K14	D25216_at	D25216	PASS	9	31.67	fail	5	9		Disease	Disease	KIAA0014		KIAA0014 gene product	KIAA0014 gene product
LTK	D16105_at	D16105	PASS	9	23.78	fail	3	9		Disease	Disease	LTK	15	leukocyte tyrosine kinase	leukocyte tyrosine kinase
K60 GNPTA	D31766_at	D31766	PASS	8	14.50	fail	6	8		Disease	Disease	KIAA0060		KIAA0060 gene product	KIAA0060 gene product
CDK2	M68520_at	M68520	PASS	8	7.63	fail	6	8		Disease	Disease	CDK2	12q13	cyclin-dependent kinase 2	cyclin-dependent kinase 2
IL11RA	U32324_at	U32324	PASS	8	9.75	fail	6	8		Disease	Disease	IL11RA	9p13	interleukin 11 receptor, alpha	interleukin 11 receptor, alpha
ACP2 ma1	X15525 ma1	X15525	PASS	8	8.75	fail	6	8		Disease	Disease	ACP2		acid phosphatase	
H326	U06631_at	U06631	PASS	8	23.13	fail	5	8		Disease	Disease	H326		homologous to mouse gene PC326:GenBank Accession Number M95564	homologous to mouse gene PC326:GenBank Accession Number M95564
TEB4	AF009301_at	AF009301	PASS	8	9.88	fail	5	8		Disease	Disease			TEB4 protein	
K170 CALT	D79992_at	D79992	PASS	8	6.88	fail	5	8		Disease	Disease	KIAA0170		KIAA0170 gene product	KIAA0170 gene product
PRKACG	M34182_at	M34182	PASS	8	41.00	fail	5	8		Disease	Disease	PRKACG	9q13	protein kinase, cAMP-dependent, catalytic, gamma	protein kinase, cAMP-dependent, catalytic, gamma
PLEC1	U53204_at	U53204	PASS	8	40.38	fail	4	8		Disease	Disease	PLEC1	8q24	plectin 1, intermediate filament binding protein, 500kD	plectin 1, intermediate filament binding protein, 500kD
E_LF113	U18009_at	U18009	PASS	8	13.00	fail	4	8		Disease	Disease			similar to Pacific ray VAT1 protein, Swiss-Prot Accession Number P19333	similar to Pacific ray VAT1 protein, Swiss-Prot Accession Number P19333
18SRNAS	AFFX-HUM1	AFFX-HUN	PASS	8	12.00	fail	3	8		Disease	Disease				
MUC3	HG2147-HT2	HG2147-H	PASS	8	60.63	fail	3	8		Disease	Disease				

H2A1B	L19778 at	L19778	PASS	6	5.00	fail	5	6	Disease	Disease	H2AFP	3p21	histone H2A.1b	H2A histone family, member P
MAP4	M64571_at	M64571	PASS	6	11.83	fail	5	6	Disease	Disease	MAP4		microtubule-associated protein 4	microtubule-associated protein 4
PML	M79462 at	M79462	PASS	6	12.00	fail	5	6	Disease	Disease	PML	15q22	promyelocytic leukemia	promyelocytic leukemia
S78798_s at	S78798_s at	S78798	PASS	6	6.50	fail	5	6	Disease	Disease			1-phosphatidylinositol-4-phosphate 5-kinase isoform C	Method: conceptual translation with partial peptide sequencing. This sequence comes from Fig. 2; PtdIns4P 5-kinase isoform C
HSD17B3	U05659_at	U05659	PASS	6	18.17	fail	5	6	Disease	Disease	HSD17B3	9q22	hydroxysteroid (17-beta) dehydrogenase 3	hydroxysteroid (17-beta) dehydrogenase 3
ASMT	U11090_at	U11090	PASS	6	11.50	fail	5	6	Disease	Disease	ASMT	Xpter-p22.32 and Yp11.3	acetylserotonin N-methyltransferase	acetylserotonin N-methyltransferase
MHC2TA	U18259 at	U18259	PASS	6	5.00	fail	5	6	Disease	Disease	MHC2TA	Chr.16	MHC class II transactivator	MHC class II transactivator
U22431_s at	U22431_s at	U22431	PASS	6	6.83	fail	5	6	Disease	Disease	HIF1A	14q21-q24	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
SNAP	U39412_at	U39412	PASS	6	16.50	fail	5	6	Disease	Disease	NAPA		N-ethylmaleimide-sensitive factor attachment protein, alpha	N-ethylmaleimide-sensitive factor attachment protein, alpha
U43189 s at	U43189 s at	U43189	PASS	6	7.17	fail	5	6	Disease	Disease	NERF-1a,b		NERF-1b	Ets transcription factor
CHM	U84720_at	U84720	PASS	6	11.83	fail	5	6	Disease	Disease	RAE1;		Homolog of yeast Rae1 (Bharathi)	homolog of yeast Rae1 (Bharathi)
ITGA6 ma1	X53586 ma1	X53586	PASS	6	8.83	fail	5	6	Disease	Disease	ITGA6	2	integrin, alpha 6	integrin, alpha 6
LY64	D83597_at	D83597	PASS	6	11.83	fail	4	6	Disease	Disease	LY64	5q12	lymphocyte antigen 64 (mouse)	lymphocyte antigen 64 (mouse)
MLLT3	L13744 at	L13744	PASS	6	5.00	fail	4	6	Disease	Disease	AF-9		homolog, radioprotective, 105kD	homolog, radioprotective, 105kD
KPNA1	S75295_at	S75295	PASS	6	5.67	fail	4	6	Disease	Disease	KPNA1		karyopherin alpha 1 (importin alpha 5)	karyopherin alpha 1 (importin alpha 5)
ZNF133	U09366 at	U09366	PASS	6	7.50	fail	4	6	Disease	Disease	ZNF169	9q22	zinc finger protein 169	zinc finger protein 169
SGSH	U30894_at	U30894	PASS	6	10.50	fail	4	6	Disease	Disease	SGSH	17q25.3	N-sulfoglucosamine sulfohydrolase (sulfamidase)	N-sulfoglucosamine sulfohydrolase (sulfamidase)
AMT	D14686_at	D14686	PASS	5	12.20	fail	6	5	Disease	Disease	AMT	3p21.2-p21.1	aminomethyltransferase (glycine cleavage system protein T)	aminomethyltransferase (glycine cleavage system protein T)
APT1LG1	D38122_at	D38122	PASS	5	5.40	fail	6	5	Disease	Disease	TNFSF6	1q23	tumor necrosis factor (ligand) superfamily, member 6	tumor necrosis factor (ligand) superfamily, member 6
K83_CHR3	D42046_at	D42046	PASS	5	6.60	fail	6	5	Disease	Disease	DNA2L	10q21.3-q22.1	DNA2 (DNA replication helicase, yeast, homolog)-like	DNA2 (DNA replication helicase, yeast, homolog)-like
TESK1	D50863 at	D50863	PASS	5	8.80	fail	6	5	Disease	Disease	TESK1	9p13	testis-specific kinase 1	testis-specific kinase 1
K172_ANK3	D79994_at	D79994	PASS	5	6.20	fail	6	5	Disease	Disease	KIAA0172		similar to ankrym of Chromatium vinosum.	similar to ankrym of Chromatium vinosum.
HG1783-HT	HG1783-HT	HG1783-H	PASS	5	4.60	fail	6	5	Disease	Disease				
HOXP12	HG2810-HT	HG2810-H	PASS	5	6.00	fail	6	5	Disease	Disease				
X104	L27476_at	L27476	PASS	5	5.20	fail	6	5	Disease	Disease	ZO-2	9q13-q21	Friedreich ataxia region gene X104 (tight junction protein ZO-2)	Friedreich ataxia region gene X104 (tight junction protein ZO-2)

BRE	L38616_at	L38616	PASS	5	11.00	fail	6	5	Disease	Disease	BRE	20q13	brain and reproductive organ-expressed (TNFRSF1A modulator)	brain and reproductive organ-expressed (TNFRSF1A modulator)
ZNF8	M29581_at	M29581	PASS	5	8.80	fail	6	5	Disease	Disease	ZNF8	20q13	zinc finger protein 8 (clone HF.18)	zinc finger protein 8 (clone HF.18)
U50648_s_at	U50648_s_at	U50648	PASS	5	24.60	fail	6	5	Disease	Disease	PRKR	2p22-p21	protein kinase, interferon-inducible double stranded RNA dependent	protein kinase, interferon-inducible double stranded RNA dependent
SCA2	U70323_at	U70323	PASS	5	12.20	fail	6	5	Disease	Disease	SCA2	12q24	ataxin 2	spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2)
ADARB1	U76421_at	U76421	PASS	5	6.20	fail	6	5	Disease	Disease	ADARB1	21q22.3	adenosine deaminase, RNA-specific, B1 (homolog of rat RED1)	adenosine deaminase, RNA-specific, B1 (homolog of rat RED1)
TSG101	U82130_at	U82130	PASS	5	7.80	fail	6	5	Disease	Disease	TSG101		tumor susceptibility protein	phosphomannomutase 1
PMM1	U86070_at	U86070	PASS	5	12.60	fail	6	5	Disease	Disease	PMM1	22q13	phosphomannomutase 1	thiosulfate sulfurtransferase (rhodanese)
TST	X59434_at	X59434	PASS	5	8.80	fail	6	5	Disease	Disease	TST		thiosulfate sulfurtransferase (rhodanese)	thiosulfate sulfurtransferase (rhodanese)
PFKP	D25328_at	D25328	PASS	5	8.60	fail	5	5	Disease	Disease	PFKP	10p15	platelet-type phosphofructokinase	phosphofructokinase, platelet
K65_ZNF118	D31763_at	D31763	PASS	5	7.60	fail	5	5	Disease	Disease	K1AA0065		ha0946 protein is Kruppel-related.	ha0946 protein is Kruppel-related.
K188_SMP2	D80010_at	D80010	PASS	5	5.40	fail	5	5	Disease	Disease	K1AA0188			
HG2809-HT2	HG2809-HT2	HG2809-HT2	PASS	5	9.80	fail	5	5	Disease	Disease				
M11025_s_a	M11025_s_a	M11025	PASS	5	6.40	fail	5	5	Disease	Disease	ASGR2	17p	asialoglycoprotein receptor 2	asialoglycoprotein receptor 2
M19267_s_a	M19267_s_a	M19267	PASS	5	7.80	fail	5	5	Disease	Disease	TPM1	15q22.1	tropomyosin 1 (alpha)	tropomyosin 1 (alpha)
TNNC1_ma	M37984_ma	M37984	PASS	5	12.80	fail	5	5	Disease	Disease	TnC		slow twitch skeletal/cardiac muscle troponin C	putative
ECGF1	S72487_at	S72487	PASS	5	10.00	fail	5	5	Disease	Disease	orf1 5' to PD-ECGF/TP			
EIF2B	U23028_at	U23028	PASS	5	8.20	fail	5	5	Disease	Disease	EIF2B5		elf-2Bepsilon	eukaryotic translation initiation factor 2B, subunit 5 (epsilon, 82kD)
CBLB	U26710_at	U26710	PASS	5	6.20	fail	5	5	Disease	Disease	CBLB	3q	Cas-Br-M (murine) ectropic retroviral transforming sequence b	Cas-Br-M (murine) ectropic retroviral transforming sequence b
ADK	U50196_at	U50196	PASS	5	5.00	fail	5	5	Disease	Disease			adenosine kinase	
ERVK_cds2	U60269_cds2	U60269	PASS	5	5.80	fail	5	5	Disease	Disease				putative polymerase; orf similar to the integrase domain of Type A and Type B retroviruses and to class II HERVs
U68162_cds1	U68162_cds1	U68162	PASS	5	6.40	fail	5	5	Disease	Disease	MPL		thrombopoietin receptor	alternative initiation codon used
POU2AF1	Z49194_at	Z49194	PASS	5	7.20	fail	5	5	Disease	Disease	POU2AF1	11q23.1	oct-binding factor	POU domain, class 2, associating factor 1
K334	AB002332_a	AB002332	PASS	5	4.80	fail	4	5	Disease	Disease	CLOCK	4q12	clock (mouse) homolog	clock (mouse) homolog
K238_PERM	D87075_at	D87075	PASS	5	6.00	fail	4	5	Disease	Disease	K1AA0238		similar to Mouse yolk sac permease like molecule 1 (U25739)	similar to Mouse yolk sac permease like molecule 1 (U25739)
K258	D87447_at	D87447	PASS	5	9.20	fail	4	5	Disease	Disease	K1AA0258		K1AA0258 gene product	K1AA0258 gene product
K279_EGFL	D87469_at	D87469	PASS	5	5.80	fail	4	5	Disease	Disease	EGFL2	chr. 1	EGF-like-domain, multiple 2	EGF-like-domain, multiple 2
AMY2B	D90097_at	D90097	PASS	5	5.60	fail	4	5	Disease	Disease	AMY2B	1p21	alpha-amylase	amylase, alpha 2B; pancreatic
M34458_ma	M34458_ma	M34458	PASS	5	5.80	fail	4	5	Disease	Disease			lamin B	lamin B

J03805_s_at	J03805_s_at	PASS	9	14.33	PASS	13	9	7.23	1.98	1.98	PPP2CB	8p12-p11.2	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
ATOX1	U70660_at	PASS	8	13.38	PASS	12	8	6.75	1.98	1.98	ATOX1	5q32-q33	ATX1 (antioxidant protein 1, yeast) homolog 1	ATX1 (antioxidant protein 1, yeast) homolog 1
K22	D14664_at	PASS	8	16.50	PASS	12	8	8.33	1.98	1.98	KIAA0022		KIAA0022 gene product	KIAA0022 gene product
SMS	Z49099_at	PASS	9	20.44	PASS	12	9	10.33	1.98	1.98	SMS	Xp22.1	spermine synthase	spermine synthase
TCTEL1	D50663_at	PASS	8	22.75	PASS	12	8	11.50	1.98	1.98	TCTEL1		similar to murine Tctel gene product	similar to murine Tctel gene product
CSTF3	U15782_at	PASS	8	11.38	PASS	12	8	5.75	1.98	1.98	CSTF3		cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD
PLI	M11119_at	PASS	7	15.00	PASS	12	7	7.58	1.98	1.98			pseudo-env cds/pseudo	pseudo-env cds/pseudo
M20867_s_a	M20867_s_a	PASS	8	14.13	PASS	13	8	7.15	1.97	1.97	GLUD1		glutamate dehydrogenase precursor (EC 1.4.1.3.)	glutamate dehydrogenase precursor (EC 1.4.1.3.)
G6PD	M24470_at	PASS	9	15.78	PASS	11	9	8.00	1.97	1.97	GMPR	6p23	glucose-6-phosphate dehydrogenase	glucose-6-phosphate dehydrogenase
K24 PTDS	D14694_at	PASS	9	41.11	PASS	13	9	20.85	1.97	1.97	KIAA0024		zinc finger; contains one C2H2 and two C4HC3	KIAA0024 gene product
REQ	U94585_at	PASS	9	19.11	PASS	13	9	9.69	1.97	1.97	hsReq		requiem homolog	requiem homolog
L19493_s_at	L19493_s_at	PASS	7	9.86	PASS	11	7	5.00	1.97	1.97	FMR1			
M12959_s_a	M12959_s_a	PASS	9	13.72	PASS	13	9	69.62	1.97	1.97	TCRA		T-cell receptor alpha-chain (VDJC)	T-cell receptor alpha-chain (VDJC)
TRSP	M86752_at	PASS	8	16.13	PASS	11	8	8.18	1.97	1.97	HEF SSP 3521		transformation-sensitive protein	
MYCBP	D89667_at	PASS	9	114.11	PASS	13	9	57.92	1.97	1.97	PFDN5		prefoldin 5	prefoldin 5
MYL6	HG2815-HT2	PASS	9	292.33	PASS	13	9	148.46	1.97	1.97				
GOK	U52426_at	PASS	7	14.00	PASS	9	7	7.11	1.97	1.97	STIM1	11p15.5	stromal interaction molecule 1	stromal interaction molecule 1
ALDH7	U34252_at	PASS	8	13.63	PASS	13	8	6.92	1.97	1.97	ALDH9	1q22-q23	aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme)	aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme)
ETFB	X71129_at	PASS	9	12.00	PASS	10	9	6.10	1.97	1.97	ETFB	19q13.3	electron-transfer-flavoprotein, beta polypeptide	electron-transfer-flavoprotein, beta polypeptide
DIPA	U63825_at	PASS	8	21.63	PASS	13	8	11.00	1.97	1.97	dipA		hepatitis delta antigen interacting protein A	hepatitis delta antigen interacting protein A
NAGA	M62783_at	PASS	9	16.44	PASS	13	9	8.38	1.96	1.96	NAGA	22q13-qter	N-acetylgalactosaminidase, alpha-	N-acetylgalactosaminidase, alpha-
K317	AB002315_a	PASS	9	11.11	PASS	12	9	5.67	1.96	1.96	KIAA0317		KIAA0317 gene product	KIAA0317 gene product
GLB1	M34423_at	PASS	9	17.11	PASS	11	9	8.73	1.96	1.96	GLB1	3p21.33	galactosidase, beta 1	galactosidase, beta 1
CDC34	L22005_at	PASS	6	12.00	PASS	8	6	6.13	1.96	1.96	CDC34	19p13.3	ubiquitin conjugating enzyme	ubiquitin conjugating enzyme
AGC1	U16306_at	PASS	9	104.11	PASS	13	9	53.15	1.96	1.96			chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide	chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide
SNRPN	J04615_at	PASS	9	51.22	PASS	13	9	26.15	1.96	1.96	SNRPN	15q12	small nuclear ribonucleoprotein polypeptide N	small nuclear ribonucleoprotein polypeptide N
ECHS1	D13900_at	PASS	9	27.00	PASS	10	9	13.80	1.96	1.96	ECHS1	10q26.2-q26.3	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial
CD14	X13334_at	PASS	9	180.11	PASS	13	9	92.08	1.96	1.96	CD14	5q22-q32	CD14 antigen	CD14 antigen
SI64	L40392_at	PASS	8	14.00	PASS	12	8	7.17	1.95	1.95			ORF; putative	ORF; putative

LRPAP1	M63959_at	M63959	PASS	8	28.25	PASS	13	8	14.46	1.95	1.95	LRPAP1	4p16.3	low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1)	low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1)
TXBP151	U33821_at	U33821	PASS	9	32.56	PASS	13	9	16.69	1.95	1.95	U33821		tax 1-binding protein	tax 1-binding protein
K177_ADPR	D79999_at	D79999	PASS	6	25.50	PASS	13	6	13.08	1.95	1.95	KIAA0177		similar to chicken poly(ADP-ribose) synthase, has putative hydrophobic domain in amino acid positions 638-662.	similar to chicken poly(ADP-ribose) synthase, has putative hydrophobic domain in amino acid positions 638-662.
MOZ	U47742_at	U47742	PASS	9	26.67	PASS	13	9	13.69	1.95	1.95	MOZ		monocytic leukaemia zinc finger protein	monocytic leukaemia zinc finger protein
HCG5	X81003_at	X81003	PASS	9	16.78	PASS	13	9	8.62	1.95	1.95	HCGV	6p21.3	hemochromatosis candidate gene V	hemochromatosis candidate gene V
J04130_s_at	J04130_s_at	J04130	PASS	9	27.56	PASS	13	9	14.15	1.95	1.95	SCYA4	17q21	small inducible cytokine A4 (homologous to mouse Mip-1b)	small inducible cytokine A4 (homologous to mouse Mip-1b)
H3F3B	M11353_at	M11353	PASS	9	245.78	PASS	13	9	126.31	1.95	1.95	H3FJ	6p22-p21.3	H3 histone family, member J	H3 histone family, member J
PSEN1	L76517_at	L76517	PASS	9	18.56	PASS	13	9	9.54	1.95	1.95	PSEN1	14q24.3	presenilin 1 (Alzheimer disease 3)	presenilin 1 (Alzheimer disease 3)
MGST2	U77604_at	U77604	PASS	8	19.00	PASS	13	8	9.77	1.94	1.94	MGST2	4q28-q31	microsomal glutathione S-transferase 2	microsomal glutathione S-transferase 2
MACS	D10522_at	D10522	PASS	8	13.75	PASS	13	8	7.08	1.94	1.94	MACS	6q21	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)
PSMHSN3	D26600_at	D26600	PASS	9	46.78	PASS	13	9	24.08	1.94	1.94	PSMB4	1q21	proteasome (prosome, macropain) subunit, beta type, 4	proteasome (prosome, macropain) subunit, beta type, 4
MYL2	M21812_at	M21812	PASS	8	11.38	PASS	7	8	5.86	1.94	1.94			myosin light chain 2	myosin light chain 2
SKI	U73377_at	U73377	PASS	9	11.44	PASS	11	9	5.91	1.94	1.94	SHC		alternatively spliced isoform in GenBank Accession Number X68148	alternatively spliced isoform in GenBank Accession Number X68148
CLK2	L29218_at	L29218	PASS	7	13.71	PASS	11	7	7.09	1.93	1.93	CLK2	1q21	CDC-like kinase 2	CDC-like kinase 2
PPBP	M54995_at	M54995	PASS	9	251.56	PASS	13	9	130.31	1.93	1.93	PPBP	4q12-q13	pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2)	pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2)
SDHA	L21936_at	L21936	PASS	9	23.44	PASS	13	9	12.15	1.93	1.93	SDHA	5p15	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
UBA52	S79522_at	S79522	PASS	9	286.56	PASS	13	9	148.69	1.93	1.93	RPS27A	2	ribosomal protein S27a	ribosomal protein S27a
SARS	X91257_at	X91257	PASS	9	38.22	PASS	13	9	19.85	1.93	1.93	serS		seryl-tRNA synthetase	seryl-tRNA synthetase
GPS2	U28963_at	U28963	PASS	8	13.63	PASS	13	8	7.08	1.93	1.93	GPS2		G protein pathway suppressor 2	G protein pathway suppressor 2
ELANH2	M93056_at	M93056	PASS	8	16.13	PASS	13	8	8.38	1.92	1.92	ELANH2	6p25	protease inhibitor 2 (anti-elastase), monocyte/neutrophil	protease inhibitor 2 (anti-elastase), monocyte/neutrophil
NT5	D38524_at	D38524	PASS	8	10.00	PASS	10	8	5.20	1.92	1.92			putative	putative
ATP50	S77356_at	S77356	PASS	9	21.00	PASS	13	9	10.92	1.92	1.92	transcript ch21		oligomycin sensitivity conferral protein oscp homolog; This sequence comes from Fig. 3. Protein sequence is in conflict with the conceptual translation; insertions(7-9, missing Y)	oligomycin sensitivity conferral protein oscp homolog; This sequence comes from Fig. 3. Protein sequence is in conflict with the conceptual translation; insertions(7-9, missing Y)
K58	D31767_at	D31767	PASS	9	108.22	PASS	13	9	56.31	1.92	1.92	KIAA0058		KIAA0058 gene product	KIAA0058 gene product

YY1	M77698 at	M77698	PASS	9	13.44	PASS	9	7.00	1.92	1.92	YY1	14q	YY1 transcription factor	YY1 transcription factor
POLR2	U37690 at	U37690	PASS	9	51.56	PASS	9	26.85	1.92	1.92	hsRBP10		RNA polymerase II subunit	
CR3p21IGS	L13434 at	L13434	PASS	6	12.00	PASS	8	6.25	1.92	1.92				
MEA	HG1869-HT	HG1869-H	PASS	9	19.33	PASS	13	10.08	1.92	1.92				
PSMC3	M34079 at	M34079	PASS	6	13.17	PASS	8	6.88	1.92	1.92	PSMC3	11p12-p13	proteasome (prosome, macropain) 26S subunit, ATPase, 3	proteasome (prosome, macropain) 26S subunit, ATPase, 3
CTGB43A	L10378 at	L10378	PASS	9	18.22	PASS	13	9.54	1.91	1.91	KIAA0084			The ha2022 gene product is novel.
K84	D42043 at	D42043	PASS	9	26.00	PASS	13	13.62	1.91	1.91				
UB ma1	U49869 ma1	U49869	PASS	9	329.78	PASS	13	173.00	1.91	1.91			ubiquitin	
CYBA	M21186 at	M21186	PASS	9	221.67	PASS	13	116.38	1.90	1.90	CYBA	16q24	cytochrome b-245, alpha polypeptide	cytochrome b-245, alpha polypeptide
PGAM1	J04173 at	J04173	PASS	9	72.56	PASS	13	38.15	1.90	1.90	PGAM1	10q25.3	phosphoglycerate mutase 1 (brain)	phosphoglycerate mutase 1 (brain)
M6PR ma1	X56253 ma1	X56253	PASS	9	46.33	PASS	13	24.38	1.90	1.90				
ITGB5	J05633 at	J05633	PASS	7	9.29	PASS	9	4.89	1.90	1.90	ITGB5		integrin, beta 5	integrin, beta 5
U68105 s at	U68105 s at	U68105	PASS	9	97.56	PASS	13	51.38	1.90	1.90				
ADAR	U10439 at	U10439	PASS	9	34.56	PASS	13	18.23	1.90	1.90	ADAR	1q21.1-q21.2	adenosine deaminase, RNA-specific	adenosine deaminase, RNA-specific
TP53BP2	U58334 at	U58334	PASS	6	12.00	PASS	12	6.33	1.89	1.89	TP53BP2	1q42.1	Bbp/53BP2	tumor protein p53-binding protein, 2
K135_PIM1	D50925 at	D50925	PASS	6	12.00	PASS	9	6.33	1.89	1.89	KIAA0135			The KIAA0135 gene is related to pim-1 oncogene.
EWSR1	X71428 at	X71428	PASS	9	72.00	PASS	13	38.00	1.89	1.89	FUS	16p11.2	FUS glycine rich protein	fusion, derived from t(12;16) malignant liposarcoma similar to Mov34
PSMD7	U70735 at	U70735	PASS	9	15.44	PASS	13	8.15	1.89	1.89				34 kDa Mov34 homolog
ZAP112	L40399 at	L40399	PASS	6	26.50	PASS	10	14.00	1.89	1.89				ORF; putative
ALOX5	J03600 at	J03600	PASS	9	29.33	PASS	12	15.50	1.89	1.89	ALOX5	10q11.2	arachidonate 5-lipoxygenase	arachidonate 5-lipoxygenase
MEN1 ma2	U93237 ma2	U93237	PASS	6	11.67	PASS	12	6.17	1.89	1.89	MEN1	11q13	multiple endocrine neoplasia 1	multiple endocrine neoplasia 1
K262	D87451 at	D87451	PASS	9	54.89	PASS	13	29.08	1.89	1.89	KIAA0262			KIAA0262 gene product
X55448 cds	X55448 cds	X55448	PASS	9	27.44	PASS	13	14.54	1.89	1.89	G6PD		glucose-6-phosphate dehydrogenase	
E_23745	U79260 at	U79260	PASS	6	12.33	PASS	11	6.55	1.88	1.88				similar to human oligodendrocyte myelin glycoprotein encoded by GenBank Accession Number L05367
CBOGS3955	D87119 at	D87119	PASS	8	19.75	PASS	12	10.50	1.88	1.88	GS3955			
BLVRA	U34877 at	U34877	PASS	8	14.88	PASS	12	7.92	1.88	1.88	BLVRA	7p14-cen	biliverdin reductase A	biliverdin reductase A
HEXB	M23294 at	M23294	PASS	6	20.67	PASS	12	11.00	1.88	1.88	HEXB	5q13	hexosaminidase B (beta polypeptide)	hexosaminidase B (beta polypeptide)
AC002045_x	AC002045_x	AC002045	PASS	9	25.00	PASS	13	13.31	1.88	1.88	A-589H1.1		Unknown protein product C1T987SK-A-589H1_1 splice form 1	
NOL1	HG1116-HT	HG1116-H	PASS	7	12.86	PASS	13	6.85	1.88	1.88				
HG2090-HT2	HG2090-HT2	HG2090-H	PASS	9	16.89	PASS	11	9.00	1.88	1.88				
NDUFA4	U94586 at	U94586	PASS	9	32.44	PASS	13	17.31	1.87	1.87	NDUFA4		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 (9kD, MLRQ)	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 (9kD, MLRQ)
K59_DMT	D31883 at	D31883	PASS	9	45.56	PASS	13	24.31	1.87	1.87	LIMAB1	10q25	LIM actin binding protein 1 (limatin)	LIM actin binding protein 1 (limatin)
3P25MP	L09260 at	L09260	PASS	9	16.11	PASS	13	8.62	1.87	1.87				

YWHAZ	M86400_at	M86400	PASS	9	116.22	PASS	9	13	9	62.15	1.87	1.87	YWHAZ	2p25.2-p25.1	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
Z74792_s_at	Z74792_s_at	Z74792	PASS	5	10.80	PASS	5	9	5	5.78	1.87	1.87			CCAAT transcription binding factor, gamma subunit	
HGB2_ma1	M91036_ma	M91036	PASS	9	60.56	PASS	9	12	9	32.42	1.87	1.87	HGB1	11p15.5	hemoglobin, gamma A	hemoglobin, gamma A
COX6B_cds	AC002115_c	AC002115	PASS	9	114.11	PASS	9	13	9	61.23	1.86	1.86	COX6B		hypothetical 36.5 kDa protein most similar to ssRNA binding proteins; BLASTX similarity to (Y07952)	hypothetical 36.5 kDa protein most similar to ssRNA binding proteins; BLASTX similarity to (Y07952)
PSMHSC10	D26598_at	D26598	PASS	9	45.56	PASS	9	13	9	24.46	1.86	1.86	PSMB3	2q35	proteasome (prosome, macropain) subunit, beta type, 3	proteasome (prosome, macropain) subunit, beta type, 3
M14328_s_a	M14328_s_a	M14328	PASS	9	173.22	PASS	9	13	9	93.15	1.86	1.86	ENO1	1p36.2-p36.3	enolase 1, (alpha)	enolase 1, (alpha)
CAPN2	M23254_at	M23254	PASS	9	63.33	PASS	9	13	9	34.08	1.86	1.86	CAPN2	1	calpain, large polypeptide L2	calpain, large polypeptide L2
HG110-HT1	HG110-HT1	HG110-HT1	PASS	9	26.44	PASS	9	13	9	14.23	1.86	1.86				
U45448_s_at	U45448_s_at	U45448	PASS	8	13.63	PASS	8	12	8	7.33	1.86	1.86	P2RX1	17p	purinergic receptor P2X, ligand-gated ion channel, 1	purinergic receptor P2X, ligand-gated ion channel, 1
K275_SPOC	D87465_at	D87465	PASS	9	50.44	PASS	9	13	9	27.15	1.86	1.86	KIAA0275	2q12-qter	KIAA0275 gene product	KIAA0275 gene product
NCL_ma1	M60858_ma	M60858	PASS	9	73.00	PASS	9	13	9	39.31	1.86	1.86	NCL		nucleolin	nucleolin
IRATHL60N	U09196_at	U09196	PASS	9	27.00	PASS	9	13	9	14.54	1.86	1.86				
CPBP	U44975_at	U44975	PASS	8	13.00	PASS	8	11	8	7.00	1.86	1.86	COPEB	10p15	core promoter element binding protein	core promoter element binding protein
ATP5G1	D13118_at	D13118	PASS	9	37.44	PASS	9	12	9	20.17	1.86	1.86	ATP5G3	2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3
EIF3	U36764_at	U36764	PASS	9	25.33	PASS	9	13	9	13.69	1.85	1.85	EIF3S2	1p34.1	eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)	eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)
XBP1	M31627_at	M31627	PASS	9	33.00	PASS	9	13	9	17.85	1.85	1.85	XBP1	22	X-box binding protein 1	X-box binding protein 1
HLA-A_f	HG3597-HT	HG3597-HT	PASS	9	182.11	PASS	9	13	9	98.62	1.85	1.85				
K77	D38521_at	D38521	PASS	9	11.67	PASS	9	12	9	6.33	1.84	1.84	KIAA0077		The ha0919 gene product is novel.	The ha0919 gene product is novel.
KPNB1	L38951_at	L38951	PASS	7	15.86	PASS	7	13	7	8.62	1.84	1.84	KPNB1		karyopherin (importin) beta 1	karyopherin (importin) beta 1
NDP52	U22897_at	U22897	PASS	9	14.22	PASS	9	11	9	7.73	1.84	1.84	ndp52		NDP52	NDP52
ARF1	M84332_at	M84332	PASS	9	115.56	PASS	9	13	9	62.85	1.84	1.84	ARF1	1q42	ADP-ribosylation factor 1	ADP-ribosylation factor 1
DAD1	D15057_at	D15057	PASS	9	20.22	PASS	9	13	9	11.00	1.84	1.84	DAD1	14q11-q12	defender against cell death 1	defender against cell death 1
PPIA_ma1	X52851_ma1	X52851	PASS	9	139.56	PASS	9	13	9	75.92	1.84	1.84			peptidylprolyl isomerase	peptidylprolyl isomerase
PPP2R56A	L42373_at	L42373	PASS	9	17.78	PASS	9	13	9	9.69	1.83	1.83	PPP2R5A	1q41	protein phosphatase 2A B56-alpha	protein phosphatase 2, regulatory subunit B (B56), alpha isoform
EIF4C	L18960_at	L18960	PASS	9	11.00	PASS	9	11	9	6.00	1.83	1.83	EIF4AY	Y chr.	eukaryotic translation initiation factor 1A, Y chromosome	eukaryotic translation initiation factor 1A, Y chromosome

GCHI	U19523_at	U19523	PASS	7	10.86	PASS	13	7	5.92	1.83	1.83	GCHI	14q22.1-q22.2	GTP cyclohydrolase I (dopa-responsive dystonia)	GTP cyclohydrolase I (dopa-responsive dystonia)
CD37	X14046_at	X14046	PASS	9	74.67	PASS	13	9	40.77	1.83	1.83	CD37	19p13-q13.4	CD37 antigen	CD37 antigen
K240	D87077_at	D87077	PASS	6	9.33	PASS	10	6	5.10	1.83	1.83	KIAA0240			
M24485_s_at	M24485_s_at	M24485	PASS	9	80.33	PASS	13	9	43.92	1.83	1.83	GSTP1	11q13	glutathione S-transferase pi	glutathione S-transferase pi
HSPD1	M22382_at	M22382	PASS	9	31.22	PASS	13	9	17.08	1.83	1.83	HSPD1		heat shock 60kD protein 1 (chaperonin)	heat shock 60kD protein 1 (chaperonin)
D26156_s_at	D26156_s_at	D26156	PASS	8	13.63	PASS	13	8	7.46	1.83	1.83	SMARCA4		SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
HLA-C f	HG658-HT63	HG658-HT	PASS	9	320.78	PASS	13	9	175.77	1.82	1.82				
HLA-E f	HG2917-HT13	HG2917-HT	PASS	9	248.00	PASS	13	9	136.00	1.82	1.82				
K34_CLTCL	D21260_at	D21260	PASS	9	23.00	PASS	13	9	12.62	1.82	1.82	CLTCL2		clathrin, heavy polypeptide-like 2	clathrin, heavy polypeptide-like 2
PRKCD	D10495_at	D10495	PASS	9	30.22	PASS	12	9	16.58	1.82	1.82	35550		protein kinase C delta-type	
M37238_s_at	M37238_s_at	M37238	PASS	9	11.33	PASS	9	9	6.22	1.82	1.82	PLCG2	16q24.1	phospholipase C, gamma 2 (phosphatidylinositol-specific)	phospholipase C, gamma 2 (phosphatidylinositol-specific)
RER1	AJ001421_at	AJ001421	PASS	9	33.89	PASS	13	9	18.62	1.82	1.82			Rer1 protein	
PPR1A	HG1614-HT1	HG1614-HT	PASS	9	106.56	PASS	13	9	58.62	1.82	1.82	PPP2R4	9q34	protein phosphatase 2A, regulatory subunit B (PR 53)	protein phosphatase 2A, regulatory subunit B (PR 53)
PPP2R4	U37352_at	U37352	PASS	7	12.57	PASS	13	7	6.92	1.82	1.82			putative alternatively spliced form of gblU63533HSU63533	putative alternatively spliced form of gblU63533HSU63533
HUNC18B2	AB002559_a	AB002559	PASS	8	21.63	PASS	11	8	11.91	1.82	1.82			prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)
J03077_s_at	J03077_s_at	J03077	PASS	9	339.89	PASS	13	9	187.54	1.81	1.81	PSAP	10q21-q22		
ARRB2	HG2059-HT2	HG2059-HT	PASS	9	24.67	PASS	13	9	13.62	1.81	1.81				
E 23652	U09011_at	U09011	PASS	9	13.00	PASS	11	9	7.18	1.81	1.81				
HG1595-HT2	HG1595-HT2	HG1595-HT	PASS	8	26.00	PASS	13	8	14.38	1.81	1.81				
CSNK1D	U29171_at	U29171	PASS	9	18.22	PASS	12	9	10.08	1.81	1.81	CSNK1D	17q25	casein kinase I, delta	casein kinase I, delta
RPS3A	M84711_at	M84711	PASS	9	298.78	PASS	13	9	165.62	1.80	1.80	RPS3A	4q31.2-q31.3	ribosomal protein S3A	ribosomal protein S3A
GLUL	X59834_at	X59834	PASS	9	23.00	PASS	12	9	12.75	1.80	1.80	GLUL	1q31	glutamate-ammonia ligase (glutamine synthase)	glutamate-ammonia ligase (glutamine synthase)
IL4R	X52425_at	X52425	PASS	9	26.22	PASS	11	9	14.55	1.80	1.80	IL4R	16p11.2-p12.1	interleukin 4 receptor	interleukin 4 receptor
CSTB mal	U46692 mal	U46692	PASS	9	47.22	PASS	13	9	26.23	1.80	1.80	CSTB	21q22.3	cystatin B (stefin B)	cystatin B (stefin B)
M22348_s_at	M22348_s_at	M22348	PASS	8	11.38	PASS	9	8	6.33	1.80	1.80	UQBP		ubiquitin-binding protein precursor	ubiquitin-binding protein precursor
RPS17	M18000_at	M18000	PASS	9	464.56	PASS	13	9	258.69	1.80	1.80	RPS17	11pter-p13 or 15q	ribosomal protein S17	ribosomal protein S17
RPLP0	M17885_at	M17885	PASS	9	436.11	PASS	13	9	243.00	1.79	1.79	RPLP0	12	ribosomal protein, large, P0	ribosomal protein, large, P0
YRS28	D14530_at	D14530	PASS	9	367.89	PASS	13	9	205.31	1.79	1.79	RPS23	5q	ribosomal protein S23	ribosomal protein S23
CBFB	L20298_at	L20298	PASS	9	21.78	PASS	13	9	12.15	1.79	1.79	CBFB	16q22.1	transcription factor	core-binding factor, beta subunit
CANX	L10284_at	L10284	PASS	9	41.89	PASS	13	9	23.38	1.79	1.79	CANX	5q35	calnexin	calnexin
HLARK	U89503_at	U89503	PASS	8	17.75	PASS	13	8	9.92	1.79	1.79	RBM4	11q13	RNA binding motif protein 4	RNA binding motif protein 4
ZFP	U69645_at	U69645	PASS	8	10.13	PASS	12	8	5.67	1.79	1.79			zinc finger protein	C2H2 type zinc finger
SUI1	L26247_at	L26247	PASS	9	177.22	PASS	13	9	99.38	1.78	1.78	sui1 iso1		isolog of yeast sui1 and rice gos2; putative	isolog of yeast sui1 and rice gos2; putative
VDAC1	L06132_at	L06132	PASS	8	15.50	PASS	13	8	8.69	1.78	1.78	VDAC1	5q31	voltage-dependent anion channel 1	voltage-dependent anion channel 1
L12711_s_at	L12711_s_at	L12711	PASS	9	67.89	PASS	13	9	38.08	1.78	1.78	TKT	3p14.3	transketolase (Wernicke-Korsakoff syndrome)	transketolase (Wernicke-Korsakoff syndrome)

EIF4A1	D13748_at	D13748	PASS	9	107.22	PASS	13	9	60.15	1.78	1.78	EIF4A1	17p13	eukaryotic translation initiation factor 4A, isoform 1
STAT13	AFEX-HUM	AFEX-HUN	PASS	9	23.44	PASS	13	9	13.15	1.78	1.78			
POLR2G_ma	U52427_ma	U52427	PASS	9	29.56	PASS	12	9	16.58	1.78	1.78	POLR2G	11q13.1	polymrase (RNA II (DNA directed) polypeptide G
M61832_s_a	M61832_s_a	M61832	PASS	7	10.29	PASS	9	7	5.78	1.78	1.78	AHCY	20cen-q13.1	S-adenosylhomocysteine hydrolase
ADPRT	J03473_at	J03473	PASS	9	17.11	PASS	13	9	9.62	1.78	1.78	ADPRT	1q41-q42	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)
HSPA9	L11066_at	L11066	PASS	9	28.33	PASS	13	9	15.92	1.78	1.78			
SMC1_xpt2	Z97054_xp2	Z97054	PASS	6	10.00	PASS	8	6	5.63	1.78	1.78			match D80000; similar to mitosis-specific chromosome; segregation protein SMC1 of S.cerevisiae
RPL34	L38941_at	L38941	PASS	9	432.56	PASS	13	9	243.62	1.78	1.78	RPL34	4 or 17	ribosomal protein L34
HLA-E_f	HG2915-HT	HG2915-H	PASS	9	245.00	PASS	13	9	138.15	1.77	1.77			
AMPHL	U68485_at	U68485	PASS	5	29.40	PASS	12	5	16.58	1.77	1.77	AMPHL	2q14	amphiphysin-like
MGAT1	M55621_at	M55621	PASS	8	18.13	PASS	13	8	10.23	1.77	1.77	MGAT1	5	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
PDHA1	D90084_at	D90084	PASS	8	10.63	PASS	9	8	6.00	1.77	1.77	PDHA1	Xp22.1	pyruvate dehydrogenase (lipoamide) alpha 1
COX4	U90915_at	U90915	PASS	9	104.44	PASS	13	9	59.00	1.77	1.77	COX4	16q22-qter	cytochrome c oxidase subunit IV
COPINE1	U83246_at	U83246	PASS	9	49.11	PASS	13	9	27.77	1.77	1.77	CPNE1		copine 1
EDG2	U11861_at	U11861	PASS	9	38.89	PASS	13	9	22.00	1.77	1.77	G10		maternal G10 transcript
K96_PK	D43636_at	D43636	PASS	9	15.89	PASS	13	9	9.00	1.77	1.77	KIAA0096		KIAA0096 gene product is related to a protein kinase.
K126_UB	D50916_at	D50916	PASS	8	13.00	PASS	11	8	7.36	1.77	1.77	UFD2	11	homolog of yeast (S. cerevisiae) ufd2
E_23682	U79288_at	U79288	PASS	8	19.13	PASS	12	8	10.83	1.77	1.77			
RPS6_ma1	M77232_ma	M77232	PASS	9	274.44	PASS	13	9	155.46	1.77	1.77	RPS6	9p21	ribosomal protein S6
GP250	U60975_at	U60975	PASS	9	63.00	PASS	13	9	35.69	1.77	1.77	SORL1	11q23.2-q24.4	sortilin-related receptor, L(DLR class) A repeats-containing
TTC3	D84294_at	D84294	PASS	9	16.56	PASS	13	9	9.38	1.76	1.76			
FYN	M14676_at	M14676	PASS	9	31.89	PASS	13	9	18.08	1.76	1.76	FYN	6q21	FYN oncogene related to SRC, FGR, YES
TUBFOLD	U61234_at	U61234	PASS	8	11.38	PASS	11	8	6.45	1.76	1.76	TBCC		tubulin-specific chaperone c
IL10R	U00672_at	U00672	PASS	9	30.22	PASS	13	9	17.15	1.76	1.76	IL10RA	11q23	interleukin 10 receptor, alpha
HG1400-HT	HG1400-HT	HG1400-H	PASS	9	11.78	PASS	13	9	6.69	1.76	1.76			
K75_E2F3	D38550_at	D38550	PASS	9	10.56	PASS	10	9	6.00	1.76	1.76	E2F3	6p22	E2F transcription factor 3
FBP1	U21931_at	U21931	PASS	9	23.67	PASS	13	9	13.46	1.76	1.76	FBP1		fructose-1,6-biphosphatase
DHPS	U79262_at	U79262	PASS	8	14.88	PASS	13	8	8.46	1.76	1.76			similar to human deoxyhypusine synthase encoded by GenBank Accession Number L39068
IGHM	X58529_at	X58529	PASS	9	112.11	PASS	13	9	63.85	1.76	1.76	IGHM	14q32.33	immunoglobulin mu
K200_MAM	D83785_at	D83785	PASS	8	12.88	PASS	12	8	7.33	1.76	1.76	KIAA0200		KIAA0200 gene product
EEF1D	Z21507_at	Z21507	PASS	9	104.11	PASS	13	9	59.31	1.76	1.76	EEF1D		eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
HG2259-HT2	HG2259-HT2	HG2259-H	PASS	9	67.44	PASS	13	9	38.54	1.75	1.75			
FUCA1	M29877_at	M29877	PASS	8	14.00	PASS	13	8	8.00	1.75	1.75	FUCA1	1p34	fucosidase, alpha-L-1, tissue

Table 1. Genes identified in the screen for genes that interact with the lymph node homing receptor precursor.

SELL	M25280_at	M25280	PASS	9	130.11	PASS	13	9	74.38	1.75	1.75	LNHR	1q12-q22	S100 calcium-binding protein A9 (calgranulin B)	lymph node homing receptor precursor
M26311_s_at	M26311_s_at	M26311	PASS	9	301.44	PASS	13	9	172.38	1.75	1.75	S100A9	1q12-q22	S100 calcium-binding protein A9 (calgranulin B)	S100 calcium-binding protein A9 (calgranulin B)
ANX2	D00017_at	D00017	PASS	9	88.33	PASS	13	9	50.62	1.75	1.75	ANX2	15q21-q22	annexin II (lipocortin II); calpactin I, heavy polypeptide	annexin II (lipocortin II); calpactin I, heavy polypeptide
K257_COSC	D87446_at	D87446	PASS	9	9.89	PASS	12	9	5.67	1.75	1.75	KIAA0257		Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)
K239_K215	D87076_at	D87076	PASS	7	19.00	PASS	10	7	10.90	1.74	1.74	KIAA0239		similar to human bromodomain protein BR140(JC2069)	similar to human bromodomain protein BR140(JC2069)
S7871_s_at	S7871_s_at	S7871	PASS	6	12.00	PASS	10	6	6.90	1.74	1.74				
X89109_s_at	X89109_s_at	X89109	PASS	9	107.22	PASS	13	9	61.69	1.74	1.74				
S82447_s_at	S82447_s_at	S82447	PASS	8	10.25	PASS	10	8	5.90	1.74	1.74	GCN5L1	12q13-q14	GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 1	GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 1
FCN1	D83920_at	D83920	PASS	9	244.89	PASS	13	9	141.00	1.74	1.74	FCN1	9q34	ficolin (collagen/fibrinogen domain-containing) 1	ficolin (collagen/fibrinogen domain-containing) 1
HLA-DMB	U15085_at	U15085	PASS	9	54.22	PASS	13	9	31.23	1.74	1.74	HLA-DMB	6p21.3	major histocompatibility complex, class II, DM beta	major histocompatibility complex, class II, DM beta
CCND2	D13639_at	D13639	PASS	9	39.11	PASS	13	9	22.54	1.74	1.74	CCND2	12p13	cyclin D2	cyclin D2
CSNK1G2	U89896_at	U89896	PASS	6	9.83	PASS	9	6	5.67	1.74	1.74			casein kinase I gamma 2	
TAF2H	U13991_at	U13991	PASS	9	33.44	PASS	13	9	19.31	1.73	1.73	tafl130		TATA-binding protein associated factor 30 kDa subunit	
M55409_s_a	M55409_s_a	M55409	PASS	9	258.78	PASS	13	9	149.46	1.73	1.73	EEF1G		eukaryotic translation elongation factor I gamma	eukaryotic translation elongation factor I gamma
W52B2_f	HG688-HT68	HG688-HT	PASS	8	61.25	PASS	13	8	35.38	1.73	1.73				
TRNASTL	U07424_at	U07424	PASS	7	14.00	PASS	11	7	8.09	1.73	1.73	FARSL		phenylalanine-tRNA synthetase like	phenylalanine-tRNA synthetase like
EIF2B	M29536_at	M29536	PASS	9	24.89	PASS	13	9	14.38	1.73	1.73	EIF2S2		eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)	eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)
E 23722	U90909_at	U90909	PASS	8	9.75	PASS	11	8	5.64	1.73	1.73				
LGALS3	M57710_at	M57710	PASS	9	66.89	PASS	13	9	38.69	1.73	1.73	LGALS3	1p13	lectin, galactoside-binding, soluble, 3 (galectin 3)	lectin, galactoside-binding, soluble, 3 (galectin 3)
PKUA	AB004884_a	AB004884	PASS	7	12.29	PASS	8	7	7.13	1.72	1.72			PKU-alpha	
J05016_ma1	J05016_ma1	J05016	PASS	8	9.88	PASS	11	8	5.73	1.72	1.72	ERP70	7; 10	protein disulfide isomerase related protein (calcium-binding, intestinal-related)	protein disulfide isomerase related protein (calcium-binding, intestinal-related)
Y09392_s_at	Y09392_s_at	Y09392	PASS	9	11.67	PASS	13	9	6.77	1.72	1.72	ws1-1		WSL-S2 protein	
U23852_s_at	U23852_s_at	U23852	PASS	9	66.89	PASS	13	9	38.85	1.72	1.72	lck		p56lck	truncated form of T-lymphocyte-specific protein tyrosine kinase p56lck; this aberrant message encoding primarily the SH2 and SH3 domains of p56lck was observed by northern hybridization and PCR amplification in poly-A selected RNA from two human leukemic T-cell lines.

P4HB	J02783_at	J02783	PASS	5	30.20	PASS	11	5	17.55	1.72	1.72	P4HB	17q25	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)
DYRK	D86550_at	D86550	PASS	9	18.67	PASS	13	9	10.85	1.72	1.72	hMNB		serine/threonine protein kinase (minibrain) gene	human homolog of Drosophila mnb (minibrain) gene
PSMC1	L02426_at	L02426	PASS	9	25.67	PASS	13	9	14.92	1.72	1.72	PSMC1	19p13.3	proteasome (prosome, macropain) 26S subunit, ATPase, 1	proteasome (prosome, macropain) 26S subunit, ATPase, 1
CD1D	L38820_at	L38820	PASS	8	12.50	PASS	11	8	7.27	1.72	1.72	CD1D		CD1D antigen	
RPL9	U09953_at	U09953	PASS	9	318.56	PASS	13	9	185.46	1.72	1.72	RPL9	4p13	ribosomal protein L9	ribosomal protein L9
U59877_s_at	U59877_s_at	U59877	PASS	6	15.67	PASS	8	6	9.13	1.72	1.72	RAB31		low-Mr GTP-binding protein Rab31	Low Mr GTP-binding protein of the Rab subfamily
GALT	M60091_at	M60091	PASS	9	11.44	PASS	9	9	6.67	1.72	1.72	GALT		galactose-1-phosphate uridylyl transferase	
MARS	X94754_at	X94754	PASS	9	13.33	PASS	13	9	7.77	1.72	1.72	MARS	12	yeast methionyl-tRNA synthetase homolog	methionine-tRNA synthetase
SI53	L40391_at	L40391	PASS	9	26.44	PASS	12	9	15.42	1.72	1.72			cyclin I	
CCNI	D50310_at	D50310	PASS	9	99.33	PASS	13	9	57.92	1.71	1.71			KIAA0099	KIAA0099 gene product
K99_PUML	D43951_at	D43951	PASS	9	12.00	PASS	11	9	7.00	1.71	1.71	KIAA0099		grancalcin	putative
SRI	M81637_at	M81637	PASS	8	9.00	PASS	8	8	5.25	1.71	1.71	grancalcin		NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase)	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase)
NDUFS8	U65579_at	U65579	PASS	6	9.00	PASS	8	6	5.25	1.71	1.71	NDUFS8	11q13		
E_23693	U79254_at	U79254	PASS	9	20.56	PASS	13	9	12.00	1.71	1.71				
K272_HYPC	D87462_at	D87462	PASS	6	11.50	PASS	7	6	6.71	1.71	1.71	BAP1	3p21.31-p21.2	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)
A4	L09604_at	L09604	PASS	9	80.22	PASS	13	9	46.85	1.71	1.71	PLP2	Xp11.23	proteolipid protein 2 (colonic epithelium-enriched)	proteolipid protein 2 (colonic epithelium-enriched)
SLC6A8_ma	U36341_ma	U36341	PASS	9	13.11	PASS	9	9	7.67	1.71	1.71	SLC6A8		creatine transporter	
TFAP3D	U91930_at	U91930	PASS	9	20.11	PASS	13	9	11.77	1.71	1.71	ADTD	19p13.3	adaptin, delta	adaptin, delta
SEPW1	U67171_at	U67171	PASS	9	25.89	PASS	13	9	15.15	1.71	1.71	SEPW1		selenoprotein W, 1	selenoprotein W, 1
P542	L38696_at	L38696	PASS	6	17.33	PASS	13	6	10.15	1.71	1.71			autoantigen p542	huRaly; hnRNP C3; N-terminus similar to huRNP C
ERCC5	X69978_at	X69978	PASS	8	12.88	PASS	9	8	7.56	1.70	1.70	ERCC5	13q22-q34	XPG complementing protein	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))
ARF4	M36341_at	M36341	PASS	9	17.56	PASS	13	9	10.31	1.70	1.70	ARF4		ADP-ribosylation factor 4	ADP-ribosylation factor 4
POLRMP	U75370_at	U75370	PASS	7	10.43	PASS	8	7	6.13	1.70	1.70	POLRMT	19p13.3	mitochondrial RNA polymerase (DNA directed)	polymrase (RNA) mitochondrial (DNA directed)
LUMAN	AF009368_at	AF009368	PASS	7	17.29	PASS	11	7	10.18	1.70	1.70			Luman	basic leucine zipper (BZIP) protein; binds to herpes simplex virus VP16 associated host cellular factor (HCF); member of CREB/ATF protein family; mouse LZIP homolog

Table 1. Summary of the results of the BLAST search for the SAP61 protein.

SAP61	U08815_at	U08815	PASS	8	10.75	PASS	9	8	6.33	1.70	1.70	SAP61	SAP61	similar to yeast PRP9, Swiss-Prot Accession Number P19736
ITK	L10717_at	L10717	PASS	9	15.67	PASS	13	9	9.23	1.70	1.70		tyrosine kinase	2024-2555 unique domain; 2556-2708 SH3 domain; 2750-3044 Sh2 domain (binds phosphotyrosine-containing proteins); 3095-3884 kinase domain (phosphorylation of tyrosine residues); putative
AFEX-HUMC	AFEX-HUMC	AFEX-HUN	PASS	7	14.14	PASS	9	7	8.33	1.70	1.70			
EIF23	U94855_at	U94855	PASS	9	60.00	PASS	13	9	35.38	1.70	1.70	EIF3S5	eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD)	eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD)
U50079_s_at	U50079_s_at	U50079	PASS	7	22.43	PASS	13	7	13.23	1.70	1.70		histone deacetylase HD1	similar to S. cerevisiae RPD3, a global transcriptional regulator; trapoxin receptor
ISG20	U88964_at	U88964	PASS	9	49.00	PASS	13	9	28.92	1.69	1.69	ISG20	interferon stimulated gene (20kD)	interferon stimulated gene (20kD)
CD81	M33680_at	M33680	PASS	9	76.22	PASS	13	9	45.00	1.69	1.69	CD81	CD81 antigen (target of antiproliferative antibody 1)	CD81 antigen (target of antiproliferative antibody 1)
U19713_s_at	U19713_s_at	U19713	PASS	9	45.33	PASS	13	9	26.77	1.69	1.69	IRT-1	interferon gamma responsive transcript	interferon gamma responsive transcript
APRT_ma1	Y00486_ma1	Y00486	PASS	9	43.22	PASS	13	9	25.54	1.69	1.69	APRT	adenine phosphoribosyltransferase	adenine phosphoribosyltransferase
NF45	U10323_at	U10323	PASS	9	24.33	PASS	13	9	14.38	1.69	1.69	ILF2	interleukin enhancer binding factor 2, 45kD	interleukin enhancer binding factor 2, 45kD
IP30	J03909_at	J03909	PASS	9	159.78	PASS	13	9	94.54	1.69	1.69			gamma-interferon-inducible protein precursor
ORF	M68864_at	M68864	PASS	9	36.78	PASS	13	9	21.77	1.69	1.69			ORF
RPL27A	U14968_at	U14968	PASS	9	369.33	PASS	13	9	218.85	1.69	1.69	RPL27A	ribosomal protein L27a	ribosomal protein L27a
RENT1	D86988_at	D86988	PASS	9	27.11	PASS	13	9	16.08	1.69	1.69	RENT1	regulator of nonsense transcripts 1	regulator of nonsense transcripts 1
MOV34L	D50063_at	D50063	PASS	9	19.11	PASS	12	9	11.33	1.69	1.69	PSMD7	16q23-q24 proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog)	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog)
FHL1	U60115_at	U60115	PASS	9	10.89	PASS	13	9	6.46	1.69	1.69	FHL1	four and a half LIM domains 1	four and a half LIM domains 1
COX5B	M19961_at	M19961	PASS	8	35.88	PASS	13	8	21.31	1.68	1.68	COX5B	cytochrome c oxidase subunit Vb	cytochrome c oxidase subunit Vb
EIF4G2	U73824_at	U73824	PASS	9	48.56	PASS	13	9	28.85	1.68	1.68	EIF4G2	eukaryotic translation initiation factor 4 gamma, 2	eukaryotic translation initiation factor 4 gamma, 2
K70_KARS	D31890_at	D31890	PASS	9	31.44	PASS	13	9	18.69	1.68	1.68	KIAA0070		similar to lysyl tRNA synthetase.
CDC37L	U43077_at	U43077	PASS	9	24.44	PASS	13	9	14.54	1.68	1.68		CDC37 homolog	similar to S. cerevisiae Cdc37p
SSBP	M94556_at	M94556	PASS	9	23.78	PASS	13	9	14.15	1.68	1.68	SSBP	single-stranded DNA-binding protein	single-stranded DNA-binding protein
RGS3	U27655_at	U27655	PASS	8	8.25	PASS	12	8	4.92	1.68	1.68		RGP3	
K190_UBP3	D80012_at	D80012	PASS	8	14.25	PASS	12	8	8.50	1.68	1.68	USP10		ubiquitin specific protease 10
FLII_ma1	U80184_ma1	U80184	PASS	7	18.43	PASS	13	7	11.00	1.68	1.68	FLII	flightless I (Drosophila) homolog	flightless I (Drosophila) homolog
AIM1	U83115_at	U83115	PASS	9	20.44	PASS	13	9	12.23	1.67	1.67	AIM1	non-lens beta gamma-crystallin like protein	absent in melanoma 1
TATSF1	U76992_at	U76992	PASS	7	10.29	PASS	13	7	6.15	1.67	1.67	Tat-SF1		similar to EWS and FUS/TLS77

K235_K99	D87078_at	D87078	PASS	5	23.40	PASS	13	5	14.00	1.67	1.67	KIAA0235			similar to D.melanogaster pumilio protein (S22026); similar to human KIAA0099 protein(D43951)
HSPB1	U12404_at	U12404	PASS	9	340.44	PASS	13	9	203.69	1.67	1.67		Csa-19		
K205_COSC	D86960_at	D86960	PASS	9	9.89	PASS	12	9	5.92	1.67	1.67	KIAA0205			KIAA0205 gene product
CTBP1	U37408_at	U37408	PASS	9	19.67	PASS	13	9	11.77	1.67	1.67	CTBP1	4p16	C-terminal binding protein 1	
EBVSRAP	HG662-HT66	HG662-HT	PASS	9	150.89	PASS	13	9	90.38	1.67	1.67				
ARHGDIB	L20688_at	L20688	PASS	9	315.00	PASS	13	9	188.69	1.67	1.67	ARHGDIB	12p12.3	GDP dissociation inhibitor	Rho GDP dissociation inhibitor (GDI) beta
LTA4H	J03459_at	J03459	PASS	9	78.78	PASS	13	9	47.23	1.67	1.67	LTA4H	12q22	leukotriene A4 hydrolase	leukotriene A4 hydrolase
ELP1	M88458_at	M88458	PASS	9	12.44	PASS	13	9	7.46	1.67	1.67				
NP220	D83032_at	D83032	PASS	9	10.00	PASS	13	9	6.00	1.67	1.67			nuclear protein, NP220	unsure initial methionine;putative
TAP	U80073_at	U80073	PASS	9	14.44	PASS	12	9	8.67	1.67	1.67	TAP		tip associating protein	
EV12B	M60830_at	M60830	PASS	8	20.25	PASS	13	8	12.15	1.67	1.67				open reading frame
K249_K188	D87436_at	D87436	PASS	8	8.88	PASS	12	8	5.33	1.66	1.66	KIAA0249			KIAA0249 gene product
CTT987SK	U95740_mal	U95740	PASS	9	14.00	PASS	12	9	8.42	1.66	1.66	A-362G6.1		Unknown gene product	
NASP	M97856_at	M97856	PASS	8	12.88	PASS	8	8	7.75	1.66	1.66	NASP		nuclear autoantigenic sperm protein (histone-binding)	nuclear autoantigenic sperm protein (histone-binding)
K94_MEAP1	D42084_at	D42084	PASS	8	11.63	PASS	13	8	7.00	1.66	1.66	KIAA0094			KIAA0094 gene product is related to S.cerevisiae methionine aminopeptidase.
L10333_s_at	L10333_s_at	L10333	PASS	5	9.80	PASS	11	5	5.91	1.66	1.66	NSP		neuroendocrine-specific protein A	
H2A1L	U90551_at	U90551	PASS	9	42.22	PASS	13	9	25.46	1.66	1.66	H2A/1		histone 2A-like protein	
K49_IAI3B	D30756_at	D30756	PASS	9	10.44	PASS	13	9	6.31	1.66	1.66	KIAA0049			KIAA0049 gene product
DNAPK	U85611_at	U85611	PASS	9	35.89	PASS	13	9	21.69	1.65	1.65	KIP		DNA-PK interaction protein	
D13720_s_at	D13720_s_at	D13720	PASS	8	14.25	PASS	13	8	8.62	1.65	1.65			ITK	originally named Jyk
K241_COST	D63877_at	D63877	PASS	6	8.50	PASS	7	6	5.14	1.65	1.65	KIAA0157			KIAA0157 gene product is novel.
RCH1	U28386_at	U28386	PASS	7	8.86	PASS	11	7	5.36	1.65	1.65	KPNA2	17q23.1-q23.3	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
K37_ADCY	D25538_at	D25538	PASS	9	17.78	PASS	13	9	10.77	1.65	1.65	ADCY7	16q12-q13	adenylate cyclase 7	adenylate cyclase 7
RS1	M24194_at	M24194	PASS	9	376.89	PASS	13	9	198.15	1.65	1.65	H12-3		MHC B complex protein 12.3	homologue; putative
IEFSSP9502	L07758_at	L07758	PASS	9	9.44	PASS	11	9	5.73	1.65	1.65			IEF SSP 9502	nuclear phosphoprotein (similarity to Saccharomyces cerevisiae PWP1 protein)
K53_CDC42	D29642_at	D29642	PASS	9	27.89	PASS	12	9	16.92	1.65	1.65	KIAA0053			KIAA0053 gene product
ABR	U01147_at	U01147	PASS	9	9.89	PASS	12	9	6.00	1.65	1.65	ABR	17p13.3	guanine nucleotide regulatory protein	active BCR-related gene
SET	M93651_at	M93651	PASS	9	24.33	PASS	13	9	14.77	1.65	1.65	SET	9q34	SET translocation (myeloid leukemia-associated)	SET translocation (myeloid leukemia-associated)
K38	D26068_at	D26068	PASS	9	54.22	PASS	13	9	32.92	1.65	1.65	WBSR1	7q11.23		Williams-Beuren syndrome chromosome region 1
PTPCAAX1	U48296_at	U48296	PASS	7	8.43	PASS	8	7	5.13	1.64	1.64	PTP4A1	6q12	Protein tyrosine phosphatase IVA1	protein tyrosine phosphatase type IVA, member 1
U01691_s_at	U01691_s_at	U01691	PASS	9	17.44	PASS	13	9	10.62	1.64	1.64	ANX5	4q28-q32	annexin V	annexin V (endonexin II)
M16591_s_at	M16591_s_at	M16591	PASS	9	29.44	PASS	13	9	17.92	1.64	1.64	HCK	20q11-q12	hemopoietic cell kinase	hemopoietic cell kinase
K102_SPC25	D14658_at	D14658	PASS	9	22.11	PASS	13	9	13.46	1.64	1.64	KIAA0102			KIAA0102 gene product
E_23815	U90916_at	U90916	PASS	8	11.88	PASS	13	8	7.23	1.64	1.64				

Table 1. Summary of the results of the BLAST search for the Nrf2 gene in the NCBI database.

NFE2L2	S74017_at	S74017	PASS	5	11.00	PASS	10	5	6.70	1.64	1.64	Nrf2	Nrf2	NF-E2-like basic leucine zipper transcriptional activator; This sequence comes from Fig. 1
MTH1	D16581_at	D16581	PASS	8	17.00	PASS	11	8	10.36	1.64	1.64	MTH1	7p22	mutT (E. coli) human homolog (8-oxo-7,8-dihydroguanosine triphosphatase)
FKHR	U36922_at	U36922	PASS	9	17.78	PASS	13	9	10.85	1.64	1.64			
K105	D14661_at	D14661	PASS	7	8.57	PASS	13	7	5.23	1.64	1.64	KIAA0105	6	gene predicted from cDNA with a complete coding sequence
CAST	D16217_at	D16217	PASS	9	20.67	PASS	13	9	12.62	1.64	1.64	CAST	5q14-q22	calpastatin
K209_DOC	D86964_at	D86964	PASS	9	20.78	PASS	13	9	12.69	1.64	1.64	DOCK2		dedicator of cyto-kinesis 2
X91911_s_at	X91911_s_at	X91911	PASS	8	21.13	PASS	13	8	12.92	1.63	1.63	rtvp-1		
DAPM	AFFX-DapX	AFFX-Dap	PASS	9	505.56	PASS	13	9	309.31	1.63	1.63			
TCF7	X59871_at	X59871	PASS	9	45.22	PASS	13	9	27.69	1.63	1.63	TCF7	5q31	transcription factor 7 (T-cell specific, HMG-box)
RPS13	HG821-HT82	HG821-HT	PASS	9	277.00	PASS	13	9	169.77	1.63	1.63			
X77588_s_at	X77588_s_at	X77588	PASS	8	10.88	PASS	12	8	6.67	1.63	1.63	ARD1	Xq28	N-acetyltransferase, homolog of S. cerevisiae ARD1
V00599_s_at	V00599_s_at	V00599	PASS	9	49.78	PASS	13	9	30.54	1.63	1.63			beta-tubulin
TP53	M22898_at	M22898	PASS	7	8.00	PASS	11	7	4.91	1.63	1.63	TP53	17p13.1	tumor protein p53 (Li-Fraumeni syndrome)
U31903_s_at	U31903_s_at	U31903	PASS	7	16.14	PASS	11	7	9.91	1.63	1.63	CREBL1	6p21.3	cAMP responsive element binding protein-like 1
SLC1A7	U53347_at	U53347	PASS	7	13.57	PASS	12	7	8.33	1.63	1.63			neutral amino acid transporter
D13413_ma	D13413_ma	D13413	PASS	9	438.11	PASS	13	9	269.08	1.63	1.63	HNRPU		heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
TGFB1	M77349_at	M77349	PASS	9	42.67	PASS	13	9	26.23	1.63	1.63	TGFB1	5q31	transforming growth factor, beta-induced, 68kD
K122	D50912_at	D50912	PASS	6	8.33	PASS	8	6	5.13	1.63	1.63	KIAA0122		The KIAA0122 gene product is novel.
AES	U04241_at	U04241	PASS	9	65.33	PASS	13	9	40.23	1.62	1.62	AES	19p13.3	amino-terminal enhancer of split
MAD3	M69043_at	M69043	PASS	9	41.33	PASS	13	9	25.46	1.62	1.62	NFKBIA	14q13	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
NME2	HG1153-HT	HG1153-HT	PASS	9	42.00	PASS	13	9	25.92	1.62	1.62			KIAA0026 gene product
K26	D14812_at	D14812	PASS	9	36.44	PASS	12	9	22.50	1.62	1.62	KIAA0026		
HG4312-HT	HG4312-HT	HG4312-HT	PASS	9	48.33	PASS	13	9	29.85	1.62	1.62			
TCRG	M30894_at	M30894	PASS	9	19.56	PASS	13	9	12.08	1.62	1.62	CD3G		Ti antigen CD3-associated protein precursor
U05572_s_at	U05572_s_at	U05572	PASS	9	27.89	PASS	13	9	17.23	1.62	1.62	MANB	19cen-q13.1	alpha-mannosidase
M98399_s_at	M98399_s_at	M98399	PASS	8	15.38	PASS	12	8	9.50	1.62	1.62	CD36	7q11.2	CD36 antigen (collagen type I receptor, thrombospondin receptor)
BLVRB	D26308_at	D26308	PASS	9	36.00	PASS	12	9	22.25	1.62	1.62	BLVRB	19q13.1-q13.2	biliverdin reductase B (flavin reductase (NADPH))
K147_ADCY	D63481_at	D63481	PASS	7	9.57	PASS	12	7	5.92	1.62	1.62	KIAA0147		biliverdin reductase B (flavin reductase (NADPH))
K115_OLIG	D29643_at	D29643	PASS	9	26.22	PASS	13	9	16.23	1.62	1.62	KIAA0115		The KIAA0147 gene product is related to adenyl cyclase.
RPL11	X79234_at	X79234	PASS	9	299.56	PASS	13	9	185.62	1.61	1.61	RPL11	1	similar to Canis oligosaccharyltransferase 48 kDa subunit (M98392).
														ribosomal protein L11

HNRPA2B1	M29064_at	M29064	PASS	9	34.00	PASS	13	9	21.08	1.61	1.61	1.61	HNRPA2B1	7p15	heterogeneous nuclear ribonucleoprotein A2/B1
PSM27	AB003177_a	AB003177	PASS	7	16.71	PASS	11	7	10.36	1.61	1.61	1.61	PSMD9	12q24.31-q24.32	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9
D42040_s_at	D42040_s_at	D42040	PASS	8	20.38	PASS	11	8	12.64	1.61	1.61	1.61	KIAA9001	11q13.3	KIAA9001 gene product
ARA9	U78521_at	U78521	PASS	9	54.56	PASS	13	9	33.85	1.61	1.61	1.61	AIP		aryl hydrocarbon receptor-interacting protein
K245_PRMA	D87432_at	D87432	PASS	8	7.88	PASS	9	8	4.89	1.61	1.61	1.61	SLC7A6		solute carrier family 7 (cationic amino acid transporter, y+ system), member 6
GMFB	AB001106_a	AB001106	PASS	7	10.14	PASS	13	7	6.31	1.61	1.61	1.61	GMFB		glia maturation factor, beta
K136	D50926_at	D50926	PASS	8	11.50	PASS	13	8	7.15	1.61	1.61	1.61	KIAA0136		The KIAA0136 gene product is novel.
BMI1	L13689_at	L13689	PASS	9	9.89	PASS	13	9	6.15	1.61	1.61	1.61	BMI1	10p13	murine leukemia viral (bmi-1) oncogene homolog
MVK	L77213_at	L77213	PASS	6	8.83	PASS	10	6	5.50	1.61	1.61	1.61			phosphomevalonate kinase
PNN	U77718_at	U77718	PASS	8	10.50	PASS	13	8	6.54	1.61	1.61	1.61	PNN		pinin, desmosome associated protein
I3KDDAP	U34343_at	U34343	PASS	9	27.67	PASS	13	9	17.23	1.61	1.61	1.61			13kD differentiation-associated protein
AF000424_s_at	AF000424_s_at	AF000424	PASS	8	68.25	PASS	13	8	42.54	1.60	1.60	1.60	LST1		cLST1/C splice variant
U72936_s_at	U72936_s_at	U72936	PASS	8	9.38	PASS	13	8	5.85	1.60	1.60	1.60	ATRX		XH2; XNP; alternatively spliced product 1; contains all exons; translation starts in exon 9; ATRX gene deposited in GenBank Accession Numbers U72900-U72935
M36429_s_at	M36429_s_at	M36429	PASS	7	15.29	PASS	13	7	9.54	1.60	1.60	1.60			transducin beta-2 subunit
EEF1B1	X60489_at	X60489	PASS	9	134.56	PASS	13	9	84.00	1.60	1.60	1.60	EEF1B2	2	eukaryotic translation elongation factor 1 beta 2
CAPZA	U56637_at	U56637	PASS	9	62.33	PASS	13	9	38.92	1.60	1.60	1.60			capping protein alpha subunit isoform 1
RPL28	U14969_at	U14969	PASS	9	444.22	PASS	13	9	277.62	1.60	1.60	1.60	RPL28	19q13.4	ribosomal protein L28
K208_DISH1	D86963_at	D86963	PASS	6	9.33	PASS	12	6	5.83	1.60	1.60	1.60	DVL3	3q27	dishevelled 3 (homologous to Drosophila dsh)
COL11A1	J04177_at	J04177	PASS	6	7.00	PASS	8	6	4.38	1.60	1.60	1.60	COL11A1	1p21	collagen, type XI, alpha 1
PD123	D14878_at	D14878	PASS	8	10.13	PASS	12	8	6.33	1.60	1.60	1.60	D123		D123 gene product
K63	D31884_at	D31884	PASS	9	11.33	PASS	11	9	7.09	1.60	1.60	1.60	KIAA0063		KIAA0063 gene product
ATP5G2_ma	X69908_ma	X69908	PASS	9	48.67	PASS	13	9	30.46	1.60	1.60	1.60	ATP5G2	12	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2
PAP	X76770_at	X76770	PASS	7	10.14	PASS	11	7	6.36	1.59	1.59	1.59			
U49835_s_at	U49835_s_at	U49835	PASS	9	13.67	PASS	12	9	8.58	1.59	1.59	1.59	CHI3L2	1p13.3	YKL-39 precursor
CDC10	S72008_at	S72008	PASS	9	32.33	PASS	13	9	20.31	1.59	1.59	1.59	CDC10		cell division cycle 10 (homologous to CDC10 of S. cerevisiae)

Table 1. List of genes and their functions.

ATP5	M37104_at	M37104	PASS	9	11.44	PASS	12	9	7.42	1.54	1.54	ATP5	10	ATP synthase, H+ transporting, mitochondrial	ATP synthase, H+ transporting, mitochondrial
ATP6E	D49400_at	D49400	PASS	9	33.11	PASS	13	9	21.46	1.54	1.54	ATP6S14	12	ATPase, vacuolar, 14 kD	ATPase, vacuolar, 14 kD
TIS11D	U07802_at	U07802	PASS	9	37.56	PASS	13	9	24.38	1.54	1.54			Tis11d	silver-stainable protein SSP29
U0439_s_at	U07439_s_at	U07439	PASS	9	87.67	PASS	13	9	56.92	1.54	1.54				similar to human PHAPI2a encoded by GenBank Accession Number Y07569 and human PHAPI2b encoded by GenBank Accession Number Y07570
CIRBP	D78134_at	D78134	PASS	9	53.89	PASS	13	9	35.00	1.54	1.54	CIRBP	19p13.3	cold inducible RNA-binding protein	cold inducible RNA-binding protein
MAD2L1	U68018_at	U68018	PASS	7	9.00	PASS	13	7	5.85	1.54	1.54	hMAD-2		mad protein homolog	
RPL30	HG2873-HT3	HG2873-H	PASS	9	487.44	PASS	13	9	317.15	1.54	1.54	ATP50	21q22.1-q22.2	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)
RPL26	HG384-HT38	HG384-HT	PASS	9	170.56	PASS	13	9	111.08	1.54	1.54				match to X98253 (NID:g2274981)
AC002477_s_at	AC002477_s	AC002477	PASS	9	13.22	PASS	13	9	8.62	1.53	1.53	ZNF183		zinc-finger protein	zinc-finger protein (PID:g2274982)
UBECS	U73379_at	U73379	PASS	5	9.20	PASS	10	5	6.00	1.53	1.53			cyclin-selective ubiquitin carrier protein	UbcH10
DECR	U49352_at	U49352	PASS	6	10.17	PASS	11	6	6.64	1.53	1.53	DECR	8q21.3	2,4-dienoyl CoA reductase	2,4-dienoyl CoA reductase
X55037_s_at	X55037_s	X55037	PASS	7	9.86	PASS	9	7	6.44	1.53	1.53	GATA3	10p15	GATA-binding protein 3	GATA-binding protein 3
IL8RB	L19593_at	L19593	PASS	5	7.80	PASS	10	5	5.10	1.53	1.53	IL8RB	2q35	interleukin 8 receptor, beta	interleukin 8 receptor, beta
TAF2D	U18062_at	U18062	PASS	9	8.67	PASS	12	9	5.67	1.53	1.53	TAF1155		TFIID subunit TAF1155	
DBI ma1	M14200_ma	M14200	PASS	8	16.00	PASS	13	8	10.46	1.53	1.53	DBI			diazepam binding inhibitor
HG4264-HT4	HG4264-HT4	HG4264-H	PASS	9	14.11	PASS	13	9	9.23	1.53	1.53			aconitase 2, mitochondrial	aconitase 2, mitochondrial
ACO2	U80040_at	U80040	PASS	8	13.75	PASS	13	8	9.00	1.53	1.53	ACO2	22q11.2-q13.31		
HLAE	X56841_at	X56841	PASS	9	140.78	PASS	13	9	92.31	1.53	1.53	HLA-E		HLA-E	
NF2TS f	HG3236-HT3	HG3236-H	PASS	9	44.22	PASS	13	9	29.00	1.52	1.52				
ACAT1	HG4073-HT4	HG4073-H	PASS	9	9.78	PASS	12	9	6.42	1.52	1.52				
S75256_s_at	S75256_s	S75256	PASS	8	10.25	PASS	11	8	6.73	1.52	1.52	HNL			neutrophil lipocalin
MNDA	M81750_at	M81750	PASS	8	41.13	PASS	13	8	27.00	1.52	1.52	MNDA	1q22	myeloid cell nuclear differentiation antigen	myeloid cell nuclear differentiation antigen
TCRB	M12886_at	M12886	PASS	9	227.67	PASS	13	9	149.69	1.52	1.52	TCRB	7q35	T-cell receptor, beta cluster	T-cell receptor, beta cluster
L09209_s_at	L09209_s	L09209	PASS	9	45.89	PASS	13	9	30.23	1.52	1.52	APLP2	11q23-q25	amyloid beta (A4) precursor-like protein 2	amyloid beta (A4) precursor-like protein 2
FTL	M11147_at	M11147	PASS	9	409.56	PASS	13	9	269.92	1.52	1.52	FTL	19q13.3-q13.4	ferritin, light polypeptide	ferritin, light polypeptide
ARD1	U14575_at	U14575	PASS	8	8.25	PASS	9	8	5.44	1.52	1.52	PPP1R8	Chr.1	protein phosphatase 1, regulatory (inhibitor) subunit 8	protein phosphatase 1, regulatory (inhibitor) subunit 8
HLA-A f	M94880_f	M94880	PASS	9	275.11	PASS	13	9	181.69	1.51	1.51				calmodulin
M19311_s_at	M19311_s	M19311	PASS	9	108.67	PASS	13	9	71.77	1.51	1.51	CSNK2B	6p21-p12	casein kinase 2, beta polypeptide	casein kinase 2, beta polypeptide
M30448_s_a	M30448_s	M30448	PASS	9	58.11	PASS	13	9	38.38	1.51	1.51				
BACTIN3	AFFX-HSAC	AFFX-HSA	PASS	9	385.33	PASS	13	9	254.54	1.51	1.51			cell surface glycoprotein	la-associated gamma chain
M13560_s_a	M13560_s	M13560	PASS	9	150.33	PASS	13	9	99.31	1.51	1.51			ribosomal protein L38	ribosomal protein L38
RBL38	Z26876_at	Z26876	PASS	9	308.11	PASS	13	9	203.62	1.51	1.51	RPL38	17	chloride intracellular channel 1	chloride intracellular channel 1
CLIC1	U93205_at	U93205	PASS	9	94.22	PASS	13	9	62.31	1.51	1.51	CLIC1		non-histone chromosomal protein	
NHC	U90549_at	U90549	PASS	5	12.40	PASS	10	5	8.20	1.51	1.51	NHC			

NPAT	D83243_at	D83243	PASS	9	9.89	PASS	11	9	6.55	1.51	1.51	NPAT	11q22-q23	nuclear protein, ataxia-telangiectasia locus	nuclear protein, ataxia-telangiectasia locus
NRNPC	M16342_at	M16342	PASS	9	25.44	PASS	13	9	16.85	1.51	1.51	HNRPC		heterogeneous nuclear ribonucleoprotein C (C1/C2)	heterogeneous nuclear ribonucleoprotein C (C1/C2)
HG1322-HT3	HG1322-HT3	HG1322-HT3	PASS	9	49.22	PASS	13	9	32.62	1.51	1.51				
SNCA	U46901_at	U46901	PASS	9	8.11	PASS	8	9	5.38	1.51	1.51	SNCA	4q21.3-q22	synuclein, alpha (non A4 component of amyloid precursor)	synuclein, alpha (non A4 component of amyloid precursor)
K5	D13630_at	D13630	PASS	8	12.75	PASS	11	8	8.45	1.51	1.51	KIAA0005		KIAA0005 gene product	KIAA0005 gene product
HDAC1	D50405_at	D50405	PASS	9	16.22	PASS	13	9	10.77	1.51	1.51	HDAC1	1p34.1	histone deacetylase 1	histone deacetylase 1
GJA4	Y08915_at	Y08915	PASS	9	19.11	PASS	13	9	12.69	1.51	1.51	IGBP1	Xq13.1-q13.3	immunoglobulin (CD79A) binding protein 1	immunoglobulin (CD79A) binding protein 1
LUC15	U23946_at	U23946	PASS	6	9.33	PASS	10	6	6.20	1.51	1.51	LUC15		putative tumor suppressor	putative tumor suppressor
VDAC2	L08666_at	L08666	PASS	9	19.89	PASS	13	9	13.23	1.50	1.50	VDAC2	10q22	voltage-dependent anion channel 2	voltage-dependent anion channel 2
M83667_ma	M83667_ma	M83667	PASS	9	42.67	PASS	13	9	28.38	1.50	1.50	NF-IL6-beta		NF-IL6-beta protein	NF-IL6-beta protein
C113	U57877_at	U57877	PASS	5	14.80	PASS	13	5	9.85	1.50	1.50	SDHC	1q21	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD
U89922_s_at	U89922_s_at	U89922	PASS	9	143.56	PASS	13	9	95.54	1.50	1.50	LTB	6p21.3	lymphotoxin beta (TNF superfamily, member 3)	lymphotoxin beta (TNF superfamily, member 3)
LYZ_ma1_f	X14008_ma1_f	X14008	PASS	9	159.22	PASS	13	9	106.00	1.50	1.50			lysosome	Protein sequence is in conflict with the conceptual translation.
NDUFV2	M22538_at	M22538	PASS	8	28.88	PASS	13	8	19.23	1.50	1.50	NDUFV2	18p11.31-p11.2	NADH-ubiquinone reductase	NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD)
L05072_s_at	L05072_s_at	L05072	PASS	9	17.56	PASS	13	9	11.69	1.50	1.50	IRF1	5q23-q31	interferon regulatory factor 1	interferon regulatory factor 1
K247	D87434_at	D87434	PASS	8	10.63	PASS	13	8	7.08	1.50	1.50	KIAA0247		KIAA0247 gene product	KIAA0247 gene product
RPS10	U14972_at	U14972	PASS	9	350.00	PASS	13	9	233.31	1.50	1.50	RPS10	6	ribosomal protein S10	ribosomal protein S10
NOT56L	Y09022_at	Y09022	PASS	8	12.13	PASS	12	8	8.08	1.50	1.50	not		Not56-like protein	Not56-like protein
BTG1	X61123_at	X61123	PASS	9	54.11	PASS	13	9	36.08	1.50	1.50	BTG1	12q22	B-cell translocation gene 1, anti-proliferative	B-cell translocation gene 1, anti-proliferative
HMOX1	X06985_at	X06985	PASS	8	32.63	PASS	13	8	21.77	1.50	1.50	HMOX1	22q12	heme oxygenase (decycling) 1	heme oxygenase (decycling) 1
RPS29	U14973_at	U14973	PASS	9	390.44	PASS	13	9	260.54	1.50	1.50	RPS29	14	ribosomal protein S29	ribosomal protein S29
PSMHSC7	D26599_at	D26599	PASS	9	24.22	PASS	12	9	16.17	1.50	1.50	PSMB2	1p34.2	proteasome (prosome, macropain) subunit, beta type, 2	proteasome (prosome, macropain) subunit, beta type, 2
SPTBN1	M96803_at	M96803	PASS	5	10.60	PASS	13	5	7.08	1.50	1.50	SPTBN1	2p21	spectrin, beta, non-erythrocytic 1	spectrin, beta, non-erythrocytic 1
K98_TCP1	D43950_at	D43950	PASS	8	17.63	PASS	13	8	11.77	1.50	1.50	KIAA0098		KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene.	KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene.
K137_COSC	D50927_at	D50927	PASS	8	10.25	PASS	13	8	6.85	1.50	1.50	KIAA0137		KIAA0137 gene product	KIAA0137 gene product
PAK1	U24152_at	U24152	PASS	9	13.22	PASS	12	9	8.83	1.50	1.50	PAK1	11q13-q14	p21/Cdc42/Rac1-activated kinase 1 (yeast Ste20-related)	p21/Cdc42/Rac1-activated kinase 1 (yeast Ste20-related)
U76764_s_at	U76764_s_at	U76764	PASS	9	38.67	PASS	13	9	25.85	1.50	1.50	CD97	19p13	CD97 antigen	CD97 antigen
X65965_s_at	X65965_s_at	X65965	PASS	9	19.44	PASS	13	9	13.00	1.50	1.50				

Table 1. CD48 protein variants and their properties.

CD48	M37766_at	M37766	PASS	9	121.67	PASS	13	9	82.38	1.48	1.48	CD48	1q21.3-q22	CD48 antigen (B-cell membrane protein)
HNRPA1	X12671_mal	X12671	PASS	9	87.11	PASS	13	9	59.00	1.48	1.48	hnrpa1 protein		CD48 antigen (B-cell membrane protein)
UBE2N	D83004_at	D83004	PASS	9	9.89	PASS	10	9	6.70	1.48	1.48	UBE2N		ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)
GTF2A2	U14193_at	U14193	PASS	8	11.13	PASS	13	8	7.54	1.48	1.48	GTF2A1		general transcription factor IIA, 1 (37kD and 19kD subunits)
TI227H	D50525_at	D50525	PASS	9	9.44	PASS	10	9	6.40	1.48	1.48			highly similar to UDP-N-acetylglucosamine transporter of K. lactis
UGALT	D87989_at	D87989	PASS	7	13.14	PASS	11	7	8.91	1.48	1.48	UGTrel1		
SAP145	U41371_at	U41371	PASS	9	17.78	PASS	11	9	12.09	1.47	1.47	SAP145		spliceosome associated protein
CMKRL1	U20350_at	U20350	PASS	9	63.78	PASS	13	9	43.38	1.47	1.47	CX3CR1	3p21	chemokine (C-X3-C) receptor 1
RPL27	L19527_at	L19527	PASS	9	320.89	PASS	13	9	218.31	1.47	1.47	RPL27	17	ribosomal protein L27
SPTAN1	J05243_at	J05243	PASS	8	8.00	PASS	9	8	5.44	1.47	1.47	SPTAN1	9q33-q34	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)
G22P1	M30938_at	M30938	PASS	9	19.78	PASS	13	9	13.46	1.47	1.47			Ku (p70/p80) subunit
MCP	X59405_at	X59405	PASS	8	9.38	PASS	13	8	6.38	1.47	1.47			
K264	D87453_at	D87453	PASS	5	7.60	PASS	11	5	5.18	1.47	1.47	KIAA0264		
SRP14	U07857_at	U07857	PASS	9	47.78	PASS	13	9	32.62	1.46	1.46	SRP14	15q22	signal recognition particle 14kD (homologous Alu RNA-binding protein)
K111_NUK3	D21853_at	D21853	PASS	9	16.00	PASS	13	9	10.92	1.46	1.46	KIAA0111		KIAA0111 gene product
IFI27SEP	J04164_at	J04164	PASS	9	227.56	PASS	13	9	155.38	1.46	1.46	IFI17		interferon-induced protein 17
RPL35	U12465_at	U12465	PASS	9	268.44	PASS	13	9	183.31	1.46	1.46			
CCT6	L27706_at	L27706	PASS	7	9.57	PASS	13	7	6.54	1.46	1.46	CCT6		chaperonin containing T-complex subunit 6
FNTA	L10413_at	L10413	PASS	9	34.33	PASS	13	9	23.46	1.46	1.46			farnesyl-protein transferase alpha-subunit
RPS9	U14971_at	U14971	PASS	9	277.78	PASS	13	9	189.85	1.46	1.46	RPS9	19q13.4	ribosomal protein S9
U09510_s_at	U09510_s_at	U09510	PASS	9	8.33	PASS	10	9	5.70	1.46	1.46	GARS	7p15	glycyl-tRNA synthetase
PECAM1	L34657_at	L34657	PASS	8	18.75	PASS	12	8	12.83	1.46	1.46	PECAM1	17q23	platelet/endothelial cell adhesion molecule (CD31 antigen)
NPC1	AF002020_at	AF002020	PASS	5	8.60	PASS	9	5	5.89	1.46	1.46	NPC1	18	Niemann-Pick disease, type C1
HSP40	D85429_at	D85429	PASS	9	21.89	PASS	13	9	15.00	1.46	1.46	HSPF1		Hsp40; Similar to bacterial DnaJ heat shock protein
PPP3CB	S46622_at	S46622	PASS	5	6.40	PASS	10	5	4.40	1.45	1.45	calcineurin A catalytic subunit		This sequence comes from Fig. 1; calmodulin-dependent protein phosphatase catalytic subunit; CaM-PP catalytic subunit
ZPK	U07358_at	U07358	PASS	7	8.86	PASS	11	7	6.09	1.45	1.45	ZPK	12q13	zipper (leucine) protein kinase
RPL12	L06505_at	L06505	PASS	9	221.67	PASS	13	9	152.46	1.45	1.45	RPL12		ribosomal protein L12
MMP1	M63483_at	M63483	PASS	5	12.60	PASS	12	5	8.67	1.45	1.45			

U45328_s_at	U45328_s_at	U45328	PASS	6	16.33	PASS	12	6	11.25	1.45	1.45	1.45	16p13.3	ubiquitin-conjugating enzyme E21 (homologous to yeast UBC9)	ubiquitin-conjugating enzyme E21 (homologous to yeast UBC9)
ACTN1	M95178_at	M95178	PASS	7	12.71	PASS	13	7	8.77	1.45	1.45	1.45	14q24	actinin, alpha 1	actinin, alpha 1
SFRS4	L14076_at	L14076	PASS	9	11.11	PASS	12	9	7.67	1.45	1.45	1.45		pre-mRNA splicing factor	SR protein family member; SR domain: (bp. 583..1529); RNA binding domains: RNP-2 (bp. 57..80) and RNP-1 (bp. 150..173)
D12775_s_at	D12775_s_at	D12775	PASS	9	7.11	PASS	11	9	4.91	1.45	1.45	1.45	11pter-p13	adenosine monophosphate deaminase (isoform E)	adenosine monophosphate deaminase (isoform E)
PF4V1_mal	M26167_mal	M26167	PASS	6	7.50	PASS	11	6	5.18	1.45	1.45	1.45	PF4var1	platelet factor 4	precursor protein
ANX4	M82809_at	M82809	PASS	6	7.83	PASS	12	6	5.42	1.45	1.45	1.45	2p13	annexin IV	annexin IV (placental anticoagulant protein II)
RPL37	HG3364-HT3	HG3364-H	PASS	9	405.56	PASS	13	9	280.62	1.45	1.45	1.45			
HLADRA	X00274_at	X00274	PASS	9	327.33	PASS	13	9	226.54	1.44	1.44	1.44		HLA-DR alpha heavy chain	Protein sequence is in conflict with the conceptual translation.
CAPZA	U03851_at	U03851	PASS	9	21.56	PASS	13	9	14.92	1.44	1.44	1.44		capping protein alpha	similar to chicken alpha2 isoform
CMPSIAT	D87969_at	D87969	PASS	9	10.11	PASS	12	9	7.00	1.44	1.44	1.44		CMP-sialic acid transporter	
ITGB7	S80335_at	S80335	PASS	9	16.44	PASS	13	9	11.38	1.44	1.44	1.44	12q13.1	integrin, beta 7	integrin, beta 7
ATP2A2	M23114_at	M23114	PASS	5	6.60	PASS	7	5	4.57	1.44	1.44	1.44	12q23-q24.1	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
J00105_s_at	J00105_s_at	J00105	PASS	9	422.56	PASS	13	9	292.69	1.44	1.44	1.44		beta-2 microglobulin	
PSMB10_cds	X71874_cds	X71874	PASS	9	73.89	PASS	13	9	51.23	1.44	1.44	1.44	16q22.1	proteasome (prosome, macropain) subunit, beta type, 10	proteasome (prosome, macropain) subunit, beta type, 10
CLARP	AF005775_at	AF005775	PASS	8	9.00	PASS	12	8	6.25	1.44	1.44	1.44	2q33-q34	CASP8 and FADD-like apoptosis regulator	CASP8 and FADD-like apoptosis regulator
NTRK1	X66397_at	X66397	PASS	9	15.22	PASS	12	9	10.58	1.44	1.44	1.44	1	translocated promoter region (to activated MET oncogene)	translocated promoter region (to activated MET oncogene)
TRA2A	U53209_at	U53209	PASS	7	22.14	PASS	10	7	15.40	1.44	1.44	1.44	htra-2 alpha	transformer-2 alpha	pre-mRNA processing factor
ATP5B	M19483_at	M19483	PASS	9	46.22	PASS	13	9	32.15	1.44	1.44	1.44	12p13-qter	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide
RPL30	HG311-HT3	HG311-HT	PASS	9	202.44	PASS	13	9	140.85	1.44	1.44	1.44			
M36430_s_at	M36430_s_at	M36430	PASS	7	12.71	PASS	13	7	8.85	1.44	1.44	1.44	1p36.21-36.33	guanine nucleotide binding protein (G protein), beta polypeptide 1	guanine nucleotide binding protein (G protein), beta polypeptide 1
IGHMBP2	V00563_at	V00563	PASS	9	42.56	PASS	13	9	29.62	1.44	1.44	1.44		reading frame (part 8) (1 is 2nd base in codon)	reading frame (part 8) (1 is 2nd base in codon)
RPL17	X55954_at	X55954	PASS	9	294.00	PASS	13	9	204.69	1.44	1.44	1.44	17q	ribosomal protein L23	ribosomal protein L23
RPL4	D23660_at	D23660	PASS	9	297.78	PASS	13	9	207.46	1.44	1.44	1.44	15	ribosomal protein L4	ribosomal protein L4
D63861_s_at	D63861_s_at	D63861	PASS	7	7.71	PASS	8	7	5.38	1.44	1.44	1.44		cyclophilin 40	
ZNF134	U09412_at	U09412	PASS	7	6.86	PASS	9	7	4.78	1.44	1.44	1.44	19q13.4	zinc finger protein 134 (clone pHZ-15)	zinc finger protein 134 (clone pHZ-15)
ATP1B3	U51478_at	U51478	PASS	9	32.11	PASS	13	9	22.38	1.43	1.43	1.43	3q22-q23	ATPase, Na+/K+ transporting, beta 3 polypeptide	ATPase, Na+/K+ transporting, beta 3 polypeptide
STX4A	U07158_at	U07158	PASS	9	11.22	PASS	12	9	7.83	1.43	1.43	1.43		syntaxin 4A (placental)	syntaxin 4A (placental)
HO3	U18937_at	U18937	PASS	8	7.88	PASS	10	8	5.50	1.43	1.43	1.43		histidyl-tRNA synthetase homologue	histidyl-tRNA synthetase homologue
CD3Z	J04132_at	J04132	PASS	9	31.56	PASS	13	9	22.08	1.43	1.43	1.43	1q22-q25	CD3Z antigen, zeta polypeptide (TIT3 complex)	CD3Z antigen, zeta polypeptide (TIT3 complex)
K41_ZNF6C	D26069_at	D26069	PASS	7	8.43	PASS	10	7	5.90	1.43	1.43	1.43			

Table 1. Genomic coordinates and gene names of the 100 genes identified in the 1000 Genomes Project.

CD79B	M89957_at	M89957	PASS	6	12.33	PASS	11	6	8.64	1.43	1.43	CD79B	17q23	cell surface glycoprotein	CD79B antigen (immunoglobulin-associated beta)
UQCRCF1	L32977_at	L32977	PASS	9	27.22	PASS	13	9	19.08	1.43	1.43	UQCRCF1		Rieske Fe-S protein	
PHC	X60036_at	X60036	PASS	9	57.89	PASS	13	9	40.62	1.43	1.43	PHC	12	phosphate carrier, mitochondrial	phosphate carrier, mitochondrial
RPS16	M60854_at	M60854	PASS	9	411.67	PASS	13	9	289.15	1.42	1.42	RPS16	19q	ribosomal protein S16	ribosomal protein S16
TMSB4	M17733_at	M17733	PASS	9	430.44	PASS	13	9	302.69	1.42	1.42	TMSB4Y	Y	thymosin, beta 4, Y chromosome	thymosin, beta 4, Y chromosome
HMGCL	L07033_at	L07033	PASS	8	7.75	PASS	11	8	5.45	1.42	1.42	HMGCL	1	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)
RPS6KA2	U08316_at	U08316	PASS	5	8.00	PASS	11	5	5.64	1.42	1.42	RPS6KA3	Xp22.2-p22.1	ribosomal protein S6 kinase, 90kD, polypeptide 3	ribosomal protein S6 kinase, 90kD, polypeptide 3
M96995_s_at	M96995_s_at	M96995	PASS	6	18.00	PASS	13	6	12.69	1.42	1.42	GRB2	17q24-q25	growth factor receptor-bound protein 2	growth factor receptor-bound protein 2
U43901_ma	U43901_ma	U43901	PASS	9	287.89	PASS	13	9	203.08	1.42	1.42			37 kD laminin receptor precursor/p40 ribosome associated protein	37LRP/p40; metastasis-associated multifunctional protein
RPL37A	L06499_at	L06499	PASS	9	428.44	PASS	13	9	302.38	1.42	1.42	RPL37A		ribosomal protein L37a	ribosomal protein L37a
GLB1	M83822_at	M83822	PASS	7	7.43	PASS	12	7	5.25	1.41	1.41	BGL		beige-like protein	similar to yeast YCR032w, GenBank Accession Number X59720, Mus musculus BG, GenBank Accession Number U52461 and C. elegans F10F2.1, GenBank Accession Number Z35598; previously identified as CDC4L
F13A1	M14539_at	M14539	PASS	9	78.00	PASS	13	9	55.15	1.41	1.41	F13A1	6p24.2-p23	coagulation factor XIII, A1 polypeptide	coagulation factor XIII, A1 polypeptide
M26708_s_at	M26708_s_at	M26708	PASS	9	183.67	PASS	13	9	130.00	1.41	1.41	PTMA		prothymosin alpha	prothymosin alpha
K02777_s_at	K02777_s_at	K02777	PASS	7	25.86	PASS	13	7	18.31	1.41	1.41	TCRA	14q11.2	T-cell receptor, alpha (V,D,J,C)	T-cell receptor, alpha (V,D,J,C)
ITRAF	U59863_at	U59863	PASS	6	6.67	PASS	11	6	4.73	1.41	1.41			I-TRAF	
RPS24L	X62691_at	X62691	PASS	9	325.00	PASS	13	9	230.46	1.41	1.41	RPS15A	16p	ribosomal protein S15a	ribosomal protein S15a
MIH1	U37547_at	U37547	PASS	7	9.71	PASS	9	7	6.89	1.41	1.41	API2	11q22	apoptosis inhibitor 2	apoptosis inhibitor 2
TRA2B	U68063_at	U68063	PASS	8	13.13	PASS	13	8	9.31	1.41	1.41	SFRS10	3q	splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10	splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10
POLR2F	Z27113_at	Z27113	PASS	9	22.33	PASS	13	9	15.85	1.41	1.41			RNA Polymerase II subunit 14.4 kD	
RPL8	Z28407_at	Z28407	PASS	9	324.56	PASS	13	9	230.46	1.41	1.41	RPL8	8	ribosomal protein L8	ribosomal protein L8
K158_DIFF6	D63878_at	D63878	PASS	8	34.13	PASS	12	8	24.25	1.41	1.41	DIFF6	2q37	differentiation 6 (deoxyguanosine triphosphate triphosphohydrolase)	differentiation 6 (deoxyguanosine triphosphate triphosphohydrolase)
M97935_s_at	M97935_s_at	M97935	PASS	9	20.44	PASS	13	9	14.54	1.41	1.41			transcription factor ISGF-3	
SI71	L40393_at	L40393	PASS	8	8.25	PASS	8	8	5.88	1.40	1.40	NUMB	14q24.3	numb (Drosophila) homolog	numb (Drosophila) homolog
HG3638-HT3	HG3638-HT3	HG3638-H	PASS	5	9.20	PASS	9	5	6.56	1.40	1.40				
K171_HYPL	D79993_at	D79993	PASS	6	7.83	PASS	12	6	5.58	1.40	1.40	KIAA0171		KIAA0171 gene product	KIAA0171 gene product
YSEC7	M85169_at	M85169	PASS	9	22.56	PASS	13	9	16.08	1.40	1.40	PSCD1	17q25	pleckstrin homology, Sec7 and coiled/coil domains 1 (cytohesin 1)	pleckstrin homology, Sec7 and coiled/coil domains 1 (cytohesin 1)
PRCP	L13977_at	L13977	PASS	9	14.67	PASS	11	9	10.45	1.40	1.40	PRCP	11q14	prolylcarboxypeptidase (angiotensinase C)	prolylcarboxypeptidase (angiotensinase C)

M4P	L03532_at	L03532	PASS	9	25.89	PASS	13	9	18.46	1.40	1.40	ARC41	M4 protein	WD repeat containing protein; similar to Sop2Hs; 41 kD subunit of the Arp2/3 protein complex
ARC41	AF006084_at	AF006084	PASS	9	88.22	PASS	13	9	62.92	1.40	1.40		p41-Arc	
K159_CHR1	D63880_at	D63880	PASS	8	7.00	PASS	9	8	5.00	1.40	1.40	KIAA0159		KIAA0159 gene product
E_POV2	U18919_at	U18919	PASS	5	6.80	PASS	7	5	4.86	1.40	1.40			
AQP3	AB001325_at	AB001325	PASS	9	20.56	PASS	13	9	14.69	1.40	1.40	AQP3	aquaporin 3	
ATP5G3	U09813_at	U09813	PASS	9	33.44	PASS	13	9	23.92	1.40	1.40	P3	mitochondrial ATP synthase subunit 9 precursor	
STAT3	L29277_at	L29277	PASS	8	10.13	PASS	12	8	7.25	1.40	1.40	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	signal transducer and activator of transcription 3 (acute-phase response factor)
CSEI1	U33286_at	U33286	PASS	8	8.75	PASS	11	8	6.27	1.39	1.39	CSEI1	chromosome segregation 1 (yeast homolog)-like	chromosome segregation 1 (yeast homolog)-like
HNRPG	Z23064_at	Z23064	PASS	9	12.33	PASS	13	9	8.85	1.39	1.39	HNRPG	heterogeneous nuclear ribonucleoprotein G	heterogeneous nuclear ribonucleoprotein G
U61397_s_at	U61397_s_at	U61397	PASS	9	9.22	PASS	13	9	6.62	1.39	1.39	UBL1	ubiquitin-like 1 (sentrin)	ubiquitin-like 1 (sentrin)
CD53	M37033_at	M37033	PASS	9	103.22	PASS	13	9	74.08	1.39	1.39	CD53	CD53 glycoprotein	CD53 antigen
RPL7A	M36072_at	M36072	PASS	9	272.56	PASS	13	9	195.62	1.39	1.39	RPL7A	ribosomal protein L7a	ribosomal protein L7a
ATP7A	AB000409_at	AB000409	PASS	9	9.89	PASS	10	9	7.10	1.39	1.39	MKNK1	MAP kinase-interacting serine/threonine kinase 1	MAP kinase-interacting serine/threonine kinase 1
RPS8_mal	X67247_mal	X67247	PASS	9	359.78	PASS	13	9	258.46	1.39	1.39	RPS8	ribosomal protein S8	ribosomal protein S8
K184	D80006_at	D80006	PASS	9	20.44	PASS	13	9	14.69	1.39	1.39	KIAA0184		
RPL6	X69391_at	X69391	PASS	9	178.33	PASS	13	9	128.23	1.39	1.39	RPL6	ribosomal protein L6	ribosomal protein L6
SHGC	M88108_at	M88108	PASS	9	22.44	PASS	13	9	16.15	1.39	1.39	p62		
K107	D14663_at	D14663	PASS	7	11.86	PASS	13	7	8.54	1.39	1.39	KIAA0107	eukaryotic translation initiation factor 3, subunit 8 (110kD)	KIAA0107 gene product
EIF3	U46025_at	U46025	PASS	9	38.33	PASS	13	9	27.62	1.39	1.39	EIF3S8		eukaryotic translation initiation factor 3, subunit 8 (110kD)
K64	D31764_at	D31764	PASS	5	14.20	PASS	13	5	10.23	1.39	1.39	KIAA0064	protein tyrosine phosphatase, non-receptor type 12	KIAA0064 gene product
PTPN12	M93425_at	M93425	PASS	9	16.22	PASS	13	9	11.69	1.39	1.39	PTPN12	N-acylsphingosine amidohydrolase	protein tyrosine phosphatase, non-receptor type 12
ACERA	U70063_at	U70063	PASS	7	13.71	PASS	9	7	9.89	1.39	1.39	ASAH	ATP binding protein	N-acylsphingosine amidohydrolase
RPL5	HG4319-HT4	HG4319-H	PASS	9	351.78	PASS	13	9	253.69	1.39	1.39		APACD:ATP binding protein associated with cell differentiation	APACD:ATP binding protein associated with cell differentiation
ATPBPCD	D64158_at	D64158	PASS	7	8.57	PASS	11	7	6.18	1.39	1.39			
S100A10	M38591_at	M38591	PASS	9	75.56	PASS	13	9	54.54	1.39	1.39	S100A10	S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))	S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))
GP25L2	X90872_at	X90872	PASS	8	15.13	PASS	13	8	10.92	1.38	1.38	gp25l2		associated to Golgi apparatus
K225_COSK	D86978_at	D86978	PASS	8	8.00	PASS	9	8	5.78	1.38	1.38	KIAA0225		similar to a C.elegans protein encoded in cosmid K12D12(Z49069)
SLC20A1	L20859_at	L20859	PASS	9	7.89	PASS	10	9	5.70	1.38	1.38	GLVRI	leukemia virus receptor 1	
U79528_s_at	U79528_s_at	U79528	PASS	9	15.00	PASS	13	9	10.85	1.38	1.38		SR31747 binding protein 1	sterol isomerase 1; SR-BP1
RPS5	U14970_at	U14970	PASS	9	293.11	PASS	13	9	212.00	1.38	1.38	RPS5	ribosomal protein S5	ribosomal protein S5
AFX-HSAC	AFX-HSAC	AFX-HSA	PASS	7	19.14	PASS	13	7	13.85	1.38	1.38			
MCM7	D55716_at	D55716	PASS	6	9.50	PASS	8	6	6.88	1.38	1.38	P1cdc47		
PBP1	U83463_at	U83463	PASS	8	10.63	PASS	13	8	7.69	1.38	1.38		scaffold protein Pbp1	

MDCR	U72342_at	U72342	PASS	9	12.11	PASS	13	9	8.77	1.38	1.38	PFAH1B1	17p13.3-p13.3	platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (45kD)	platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (45kD)
RPI	L35035_at	L35035	PASS	8	7.25	PASS	8	8	5.25	1.38	1.38				
UBE2D2	U39317_at	U39317	PASS	9	14.22	PASS	13	9	10.31	1.38	1.38	UBE2D3		ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)
DDX	U90426_at	U90426	PASS	9	11.67	PASS	13	9	8.46	1.38	1.38			nuclear RNA helicase	DEAD-box family member; contains DEAD-box; similar to rat liver nuclear protein p47 (PIR Accession Number A42881) and D. melanogaster DEAD-box RNA helicase WM6 (PIR Accession Number S51601)
RPS25	M64716_at	M64716	PASS	9	275.67	PASS	13	9	200.15	1.38	1.38	RPS25	11q23.3	ribosomal protein S25	ribosomal protein S25
PSMB8_ma	Z14982_ma	Z14982	PASS	8	30.75	PASS	12	8	22.33	1.38	1.38	MHC-encoded proteasome subunit gene		proteasome subunit LMP7	alternative splicing
HG3730-HT4	HG3730-HT4	HG3730-H	PASS	8	9.75	PASS	12	8	7.08	1.38	1.38				
RPL21	U25789_at	U25789	PASS	9	153.78	PASS	13	9	111.77	1.38	1.38	RPL21	13	ribosomal protein L21	ribosomal protein L21
DUT	U31930_at	U31930	PASS	9	11.11	PASS	13	9	8.08	1.38	1.38	DUT	15q15-q21.1	dUTP pyrophosphatase	dUTP pyrophosphatase
EIF4G2	D86549_at	D86549	PASS	8	6.88	PASS	11	8	5.00	1.38	1.38			p97 homologous protein	
K232	D86985_at	D86985	PASS	6	7.00	PASS	11	6	5.09	1.38	1.38	KIAA0232		KIAA0232 gene product	KIAA0232 gene product
PGD	U30255_at	U30255	PASS	6	22.00	PASS	10	6	16.00	1.38	1.38	PGD	1p36.3-p36.13	phosphogluconate dehydrogenase	phosphogluconate dehydrogenase
EMAPII	U10117_at	U10117	PASS	9	10.11	PASS	11	9	7.36	1.37	1.37	EMAPII		endothelial-monocyte activating polypeptide II	endothelial-monocyte activating polypeptide II
DSSI	U41515_at	U41515	PASS	9	8.78	PASS	10	9	6.40	1.37	1.37	DSSI		Method: conceptual translation supplied by author.	Method: conceptual translation supplied by author.
M14199_s_a	M14199_s_a	M14199	PASS	9	302.00	PASS	13	9	220.23	1.37	1.37	LAMR1	3p21.3	laminin receptor 1 (67kD); Ribosomal protein SA	laminin receptor 1 (67kD); Ribosomal protein SA
STXBP3	D63506_at	D63506	PASS	9	10.33	PASS	13	9	7.54	1.37	1.37	Munc-18-3		unc-18homologue	unc-18homologue
NME1	X17620_at	X17620	PASS	8	8.38	PASS	9	8	6.11	1.37	1.37	NME1	17q22	non-metastatic cells 1, protein (NM23A) expressed in	non-metastatic cells 1, protein (NM23A) expressed in
RPL3	X73460_at	X73460	PASS	9	364.22	PASS	13	9	265.77	1.37	1.37	RPL3	22	ribosomal protein L3	ribosomal protein L3
APEX	D13370_at	D13370	PASS	9	20.44	PASS	13	9	14.92	1.37	1.37	APEX	14q11.2-q12	APEX nuclease (multifunctional DNA repair	APEX nuclease (multifunctional DNA repair enzyme)
K201_HSP10	D86956_at	D86956	PASS	6	7.00	PASS	9	6	5.11	1.37	1.37	KIAA0201		KIAA0201 gene product	KIAA0201 gene product
COX10_ma	U82010_ma	U82010	PASS	9	8.56	PASS	12	9	6.25	1.37	1.37	COX10	17p12-p11.2	cytochrome c oxidase subunit X (heme A: farnesyltransferase)	cytochrome c oxidase subunit X (heme A: farnesyltransferase)
LYZ_f	M19045_f_at	M19045	PASS	9	155.67	PASS	13	9	113.77	1.37	1.37	LYZ		lysozyme precursor (EC 3.2.1.17)	lysozyme precursor (EC 3.2.1.17)
RPL19	X63527_at	X63527	PASS	9	379.44	PASS	13	9	277.54	1.37	1.37	RPL19	17p12-q11	ribosomal protein L19	ribosomal protein L19
DPYD	U20938_at	U20938	PASS	8	9.25	PASS	13	8	6.77	1.37	1.37			dihydropyrimidine dehydrogenase	DPD; dihydrouracil dehydrogenase
Z47055_s_at	Z47055_s_at	Z47055	PASS	9	9.22	PASS	12	9	6.75	1.37	1.37	FDPS		farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)

LYN	M16038_at	M16038	PASS	9	17.11	PASS	13	9	12.54	1.36	LYN	8q13	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
hum alu at	hum alu at	hum	PASS	9	422.44	PASS	13	9	309.62	1.36			v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
PCM1	L27841_at	L27841	PASS	6	7.83	PASS	8	6	5.75	1.36	PCM-1		pericentriol material 1
ACAA	D16294_at	D16294	PASS	8	9.13	PASS	10	8	6.70	1.36			mitochondrial 3-oxoacyl-CoA thiolase
PSMA3	D00760_at	D00760	PASS	8	11.00	PASS	12	8	8.08	1.36	PSMA2	6q27	proteasome (prosome, macropain) subunit, alpha type, 2
U07806_s_at	U07806_s_at	U07806	PASS	8	11.25	PASS	11	8	8.27	1.36			DNA topoisomerase 1
A82KD	U15552_at	U15552	PASS	7	8.71	PASS	12	7	6.42	1.36			acidic 82 kDa protein
D26535_s_at	D26535_s_at	D26535	PASS	8	10.00	PASS	11	8	7.36	1.36	DLST	14q24.3	dihydroipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)
Z49148_s_at	Z49148_s_at	Z49148	PASS	9	285.33	PASS	13	9	210.23	1.36	RPL29	3q29-qter	ribosomal protein L29
EED	U90651_at	U90651	PASS	7	8.14	PASS	11	7	6.00	1.36	BED	11q14.2-q22.3	embryonic ectoderm development protein
DYRK2	Y09216_at	Y09216	PASS	6	10.17	PASS	12	6	7.50	1.36	DYRK2	12	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
LLREP3	X17206_at	X17206	PASS	9	471.00	PASS	13	9	347.46	1.36	RPS2	16p13.3	ribosomal protein S2
UBA52_ma	X56997_ma	X56997	PASS	9	268.44	PASS	13	9	198.08	1.36	UBA52		ubiquitin-52 amino acid fusion protein
RPS18	X69150_at	X69150	PASS	9	377.78	PASS	13	9	278.77	1.36	RPS18	6p21.3	ribosomal protein S18
FCER2	M15059_at	M15059	PASS	9	9.33	PASS	9	9	6.89	1.35	FCER2	19p13.3	Fc fragment of IgE, low affinity II, receptor for (CD231A)
P87	L42572_at	L42572	PASS	8	8.38	PASS	11	8	6.18	1.35	p87/89		transmembrane protein
BTK_ma4	U78027_ma4	U78027	PASS	7	10.71	PASS	12	7	7.92	1.35	FTP3		lysosomal exoglycosidase
HCG8	X92110_at	X92110	PASS	5	5.80	PASS	7	5	4.29	1.35			
PSKH1	U09564_at	U09564	PASS	8	7.50	PASS	11	8	5.55	1.35	SRPK1	6p21.2-p21.3	SFRS protein kinase 1
U09820_s_at	U09820_s_at	U09820	PASS	7	8.71	PASS	9	7	6.44	1.35	ATRX	Xq13.1-q21.1	alpha thalassemia/mental retardation syndrome X-linked helicase II
U37546_s_at	U37546_s_at	U37546	PASS	8	7.13	PASS	11	8	5.27	1.35	API1	11q22	apoptosis inhibitor 1
S54005_s_at	S54005_s_at	S54005	PASS	9	184.44	PASS	13	9	136.54	1.35	thymosin beta-10		This sequence comes from Fig. 1.
LKYHYD	U57721_at	U57721	PASS	9	9.44	PASS	13	9	7.00	1.35	KYNU		kynureninase; l-kynurenine hydrolase
X95325_s_at	X95325_s_at	X95325	PASS	5	21.80	PASS	12	5	16.17	1.35	dbpAv		variant A
RARS	S80343_at	S80343	PASS	8	7.50	PASS	7	8	5.57	1.35	RARS	5pter-q11	arginyl-tRNA synthetase
K148	D63482_at	D63482	PASS	5	7.80	PASS	10	5	5.80	1.34	K1AA0148		K1AA0148 gene product
K178_SMC1	D80000_at	D80000	PASS	6	6.17	PASS	10	6	4.60	1.34	K1AA0178		similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae.
RPS11	X06617_at	X06617	PASS	9	380.22	PASS	13	9	284.08	1.34	RPS11	19q13.3	ribosomal protein S11
JUN	U65928_at	U65928	PASS	8	8.75	PASS	11	8	6.55	1.34	JUN	1p32-p31	v-jun avian sarcoma virus 17 (v-jun) oncogene homolog
INT6	U62962_at	U62962	PASS	9	52.67	PASS	13	9	39.46	1.33	EIF3S6	8q22-q23	murine mammary tumor integration site 6 (oncogene homolog)
RSU1	L12535_at	L12535	PASS	9	13.44	PASS	13	9	10.08	1.33	RSU-1		homologous to mouse Rsu-1; putative

Table 1. Genes and proteins associated with the 13q33.3 deletion syndrome.

SFRS7_ma1	L41887_ma1	L41887	PASS	6	6.33	PASS	8	6	4.75	1.33	1.33	SFRS7		splicing factor, arginine/serine-rich 7	35 kDa protein
K71	D31888_at	D31888	PASS	8	7.25	PASS	9	8	5.44	1.33	1.33	KIAA0071			
ANT3	J03592_at	J03592	PASS	9	200.78	PASS	13	9	151.00	1.33	1.33	ANT3	Xp22.32		adenine nucleotide translocator 3 (liver)
MDH1	D55654_at	D55654	PASS	9	25.56	PASS	13	9	19.23	1.33	1.33				
RPLP2	AB002533_a	AB002533	PASS	9	355.11	PASS	13	9	267.23	1.33	1.33	KPNA4			karyopherin alpha 4 (importin alpha 3)
PSMA5	D00761_at	D00761	PASS	9	33.11	PASS	13	9	24.92	1.33	1.33	PSMB1	7p13-p12		proteasome (prosome, macropain) subunit, beta type, 1
NPM1	M23613_at	M23613	PASS	9	103.33	PASS	13	9	77.85	1.33	1.33	NPM1	5q35		nucleophosmin
K2 TRIC5	D13627_at	D13627	PASS	9	15.78	PASS	12	9	11.92	1.32	1.32	KIAA0002			nucleophosmin (nucleolar phosphoprotein B23, numatrin)
GZMK	U26174_at	U26174	PASS	6	17.50	PASS	13	6	13.23	1.32	1.32	GZMK			KIAA0002 gene product
MRP	X78338_at	X78338	PASS	7	7.43	PASS	8	7	5.63	1.32	1.32				granzyme K (serine protease, granzyme 3; tryptase II)
M16336_s_a	M16336_s_a	M16336	PASS	9	52.11	PASS	13	9	39.54	1.32	1.32	CD2	1p13		CD2 antigen (p50), sheep red blood cell receptor
K164 DNABD	D79986_at	D79986	PASS	8	16.63	PASS	13	8	12.62	1.32	1.32	KIAA0164			KIAA0164 gene product
RPL17	X53777_at	X53777	PASS	9	206.44	PASS	13	9	156.69	1.32	1.32	RPL17	18q		ribosomal protein L17
SPHAR ma1	X82554_ma1	X82554	PASS	5	6.00	PASS	9	5	4.56	1.32	1.32	SPHAR			ribosomal protein L17
SRC1	U59302_at	U59302	PASS	9	11.44	PASS	13	9	8.69	1.32	1.32	SRC1	2p23		steroid receptor coactivator 1
FLI1	M98833_at	M98833	PASS	7	8.29	PASS	13	7	6.31	1.31	1.31	FLI1	11q24.1-q24.3		Friend leukemia virus integration 1
K16	D13641_at	D13641	PASS	8	13.13	PASS	13	8	10.00	1.31	1.31	KIAA0016			mitochondrial outer membrane protein 19
TFAP3S	U91932_at	U91932	PASS	9	14.33	PASS	13	9	10.92	1.31	1.31	CLAPS3	12p13.2-p13.1		clathrin-associated/assembly/adaptor protein, small 3 (22kD)
GUASMPST	HG4716-HT3	HG4716-H	PASS	8	7.75	PASS	11	8	5.91	1.31	1.31				
RPS28	U58682_at	U58682	PASS	9	286.67	PASS	13	9	218.69	1.31	1.31	RPS28	19p13.2		ribosomal protein S28
RAB11A	AF000231_at	AF000231	PASS	6	6.17	PASS	7	6	4.71	1.31	1.31				GTPase
AFFX-HUMC	AFFX-HUMC	AFFX-HUN	PASS	6	12.17	PASS	13	6	9.31	1.31	1.31	HPRT1	Xq26.1		hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)
HPRT1	M31642_at	M31642	PASS	8	7.63	PASS	12	8	5.83	1.31	1.31				hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)
PSM112	D44466_at	D44466	PASS	9	7.44	PASS	10	9	5.70	1.31	1.31	PSMD1			proteasome (prosome, macropain) 26S subunit, non-ATPase, 1
PEBP2AC1	Z35278_at	Z35278	PASS	9	19.78	PASS	13	9	15.15	1.31	1.31	CBFA3	1p36		core-binding factor, runt domain, alpha subunit 3
PSMCP31	D38047_at	D38047	PASS	9	31.22	PASS	13	9	23.92	1.31	1.31	PSMD8			proteasome (prosome, macropain) 26S subunit, non-ATPase, 8
PSM42	D78275_at	D78275	PASS	8	9.25	PASS	10	8	7.10	1.30	1.30	PSMC6	12q15		proteasome (prosome, macropain) 26S subunit, ATPase, 6
P76	U81006_at	U81006	PASS	7	9.00	PASS	11	7	6.91	1.30	1.30	P76			76 kDa membrane protein
K54 MOV10	D29677_at	D29677	PASS	7	8.29	PASS	11	7	6.36	1.30	1.30	KIAA0054			KIAA0054 gene product
SKIP	U51432_at	U51432	PASS	6	13.00	PASS	10	6	10.00	1.30	1.30				nuclear protein Skip

Table 1. List of genes and their products.

K256	D87445_at	D87445	PASS	6	6.50	PASS	9	6	5.00	1.30	1.30	KIAA0256		KIAA0256 gene product
LGALS8	L78132_at	L78132	PASS	6	6.17	PASS	8	6	4.75	1.30	1.30	beta-1	prostate carcinoma tumor antigen	
POLR2	U37689_at	U37689	PASS	5	9.80	PASS	9	5	7.56	1.30	1.30	hsRBP8	RNA polymerase II subunit	
CASP10	U60519_at	U60519	PASS	6	6.67	PASS	7	6	5.14	1.30	1.30	CASP10	caspase 10, apoptosis-related cysteine protease	
L14778_s_at	L14778_s_at	L14778	PASS	9	9.78	PASS	11	9	7.55	1.30	1.30	PPP3CA	calmodulin-dependent phosphatase catalytic subunit	caspase 10, apoptosis-related cysteine protease
RAB ma1	L42025_ma1	L42025	PASS	6	6.33	PASS	9	6	4.89	1.30	1.30	HRB	HIV-1 Rev binding protein	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)
GAPDHM	AFFX-HUM0	AFFX-HUM0	PASS	9	162.00	PASS	13	9	125.31	1.29	1.29			HIV-1 Rev binding protein
E 121711DN	U92014_at	U92014	PASS	6	6.83	PASS	7	6	5.29	1.29	1.29			
HRMT1L1	X99209_at	X99209	PASS	9	20.78	PASS	13	9	16.08	1.29	1.29		arginine methyltransferase	
RPL10	HG4542-HT4	HG4542-H	PASS	9	184.78	PASS	13	9	143.08	1.29	1.29			
28SRNA5	AFFX-M278	AFFX-M27	PASS	7	8.71	PASS	8	7	6.75	1.29	1.29			
YWHA	X56468_at	X56468	PASS	9	23.33	PASS	13	9	18.08	1.29	1.29		14.3.3 protein	
ACADM	M91432_at	M91432	PASS	8	7.50	PASS	11	8	5.82	1.29	1.29	ACADM	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain
PMR1	U25165_at	U25165	PASS	7	11.00	PASS	13	7	8.54	1.29	1.29	FXR1	FXR1	fragile X mental retardation, autosomal homolog 1
HMG17_ma	X13546_ma1	X13546	PASS	9	40.22	PASS	13	9	31.23	1.29	1.29	HMG17	put. HMG-17 protein	high-mobility group (nonhistone chromosomal) protein 17
K6_VAV1	D25304_at	D25304	PASS	9	16.11	PASS	13	9	12.54	1.28	1.28	KIAA0006		PAK-interacting exchange factor alpha
SNRPD2	U15008_at	U15008	PASS	9	140.33	PASS	13	9	109.23	1.28	1.28	SNRPD2	small nuclear ribonucleoprotein D2 polypeptide (16.5kD)	small nuclear ribonucleoprotein D2 polypeptide (16.5kD)
COX5A	M22760_at	M22760	PASS	9	16.89	PASS	13	9	13.15	1.28	1.28	COX5A	cytochrome c oxidase subunit Va	cytochrome c oxidase subunit Va
VRK1	AB000449_a	AB000449	PASS	7	7.57	PASS	10	7	5.90	1.28	1.28	VRK1	vaccinia related kinase 1	vaccinia related kinase 1
M31516_s_a	M31516_s_a	M31516	PASS	5	6.20	PASS	12	5	4.83	1.28	1.28	DAF	decay-accelerating factor	decay accelerating factor for complement (CD55, Crimer blood group system)
TRPOS1	M23161_at	M23161	PASS	7	6.29	PASS	11	7	4.91	1.28	1.28			
PSMCS	L38810_at	L38810	PASS	9	14.67	PASS	11	9	11.45	1.28	1.28	PSMCS	proteasome (prosome, macropain) 26S subunit, ATPase, 5	proteasome (prosome, macropain) 26S subunit, ATPase, 5
UROD	M14016_at	M14016	PASS	7	7.86	PASS	7	7	6.14	1.28	1.28	UROD	uroporphyrinogen decarboxylase	uroporphyrinogen decarboxylase
POLR2	HG2274-HT4	HG2274-H	PASS	6	10.33	PASS	12	6	8.08	1.28	1.28			
M96954_s_a	M96954_s_a	M96954	PASS	9	7.67	PASS	13	9	6.00	1.28	1.28		nucleolysin TIAR	
TRP185	U38847_at	U38847	PASS	5	6.20	PASS	7	5	4.86	1.28	1.28	TRP-185	TAR RNA loop binding protein	TRP-185
GCNT1	U77413_at	U77413	PASS	5	7.40	PASS	10	5	5.80	1.28	1.28	OGT	O-GlcNAc transferase (uridine diphospho-N-acetylglucosamine:polypeptide beta-N-acetylglucosaminyl transferase)	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
RAN	HG1112-HT	HG1112-H	PASS	9	21.44	PASS	13	9	16.85	1.27	1.27			
INDPOLAB	U33818_at	U33818	PASS	8	14.88	PASS	13	8	11.69	1.27	1.27	IPABP	inducible poly(A)-binding protein	inducible poly(A)-binding protein
DPM1	AF007875_a	AF007875	PASS	8	8.38	PASS	12	8	6.58	1.27	1.27	DPM1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit

Table 1. Genes and proteins associated with the 19q13.1-q13.2 deletion syndrome.

TCF3	M31523_at	M31523	PASS	9	6.89	PASS	12	9	5.42	1.27	1.27	TCF3	19		transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)
Z26491_s_at	Z26491_s_at	Z26491	PASS	9	13.89	PASS	13	9	10.92	1.27	1.27				
HNRNPCL	M94630_at	M94630	PASS	9	27.56	PASS	13	9	21.69	1.27	1.27	HNRPD	4q21		heterogeneous nuclear ribonucleoprotein D
K212_COSC	D86967_at	D86967	PASS	7	11.43	PASS	12	7	9.00	1.27	1.27	KIAA0212			KIAA0212 gene product
EIF2A	U26032_at	U26032	PASS	5	5.80	PASS	7	5	4.57	1.27	1.27				
TGFBR2	D50683_at	D50683	PASS	9	24.00	PASS	13	9	18.92	1.27	1.27	TGFBR2	3p22		transforming growth factor, beta receptor II (70-80kD)
PPP2R2A	M64929_at	M64929	PASS	7	7.29	PASS	8	7	5.75	1.27	1.27	PPP2R2A			protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform
GPRK5	L15388_at	L15388	PASS	6	6.33	PASS	7	6	5.00	1.27	1.27	GPRK5	10q24-qter		G protein-coupled receptor kinase 5
PPP3CB2	M29551_at	M29551	PASS	5	7.60	PASS	9	5	6.00	1.27	1.27				calcineurin A2
HG3484-HT	HG3484-HT	HG3484-H	PASS	7	8.86	PASS	12	7	7.00	1.27	1.27				
CCNH	U11791_at	U11791	PASS	7	6.43	PASS	12	7	5.08	1.26	1.26	CCNH	5q13.3-q14		cyclin H
H2B_ma2	X57985_ma2	X57985	PASS	9	9.11	PASS	13	9	7.23	1.26	1.26	H2AFQ	1q21-q23		H2A histone family, member Q
NFKB1	M38603_at	M38603	PASS	6	16.17	PASS	12	6	12.83	1.26	1.26	NFKB1	4q24		nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)
G22P1	J04611_at	J04611	PASS	9	23.44	PASS	13	9	18.62	1.26	1.26	G22P1	22q11.1-q13		thyroid autoantigen 70kD (Ku antigen)
RABGGTB	X98001_at	X98001	PASS	6	6.67	PASS	10	6	5.30	1.26	1.26	RABGGTB	1p31-p22		Rab geranylgeranyltransferase, beta subunit
ECH1	U16660_at	U16660	PASS	7	20.57	PASS	13	7	16.38	1.26	1.26	ECH1	19q13.1		enoyl Coenzyme A hydratase 1, peroxisomal
K276_HYPL	D87466_at	D87466	PASS	7	5.71	PASS	9	7	4.56	1.25	1.25	KIAA0276			Similar to S.cerevisiae hypothetical protein L3111 (S59316)
K78_RAD21	D38551_at	D38551	PASS	8	10.63	PASS	12	8	8.50	1.25	1.25	RAD21			RAD21 (S. pombe) homolog
ECGF1	M31210_at	M31210	PASS	8	6.38	PASS	10	8	5.10	1.25	1.25	EDG1	1pter-qter		endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
M58525_s_at	M58525_s_at	M58525	PASS	5	10.40	PASS	12	5	8.33	1.25	1.25	COMT	22q11.21-q11.23		catechol-O-methyltransferase
HG2639-HT	HG2639-HT	HG2639-H	PASS	9	11.89	PASS	13	9	9.54	1.25	1.25				
ZNF43_f	X59244_f_at	X59244	PASS	5	5.60	PASS	10	5	4.50	1.24	1.24	ZNF43	19p13.1-p12		zinc finger protein 43 (HTF6)
D79984_s_at	D79984_s_at	D79984	PASS	5	6.40	PASS	7	5	5.14	1.24	1.24	KIAA0162			similar to emb-5 protein of C.elegans.
MIF_ma1	L19686_ma1	L19686	PASS	9	43.33	PASS	13	9	34.85	1.24	1.24	MIF	22q11.2		macrophage migration inhibitory factor (glycosylation-inhibiting factor)
CBF	M37197_at	M37197	PASS	8	6.75	PASS	7	8	5.43	1.24	1.24	CEBP			CCAAT-box-binding factor
M90391_s_at	M90391_s_at	M90391	PASS	7	7.71	PASS	9	7	6.22	1.24	1.24	IL16			interleukin 16 (lymphocyte chemoattractant factor)
K29	D21852_at	D21852	PASS	9	7.33	PASS	12	9	5.92	1.24	1.24	KIAA0029			
CTSS	M90696_at	M90696	PASS	8	12.38	PASS	11	8	10.00	1.24	1.24	CTSS	1q21		cathepsin S
X15673_s_at	X15673_s_at	X15673	PASS	5	9.40	PASS	10	5	7.60	1.24	1.24				
ERH	D85758_at	D85758	PASS	7	21.86	PASS	13	7	17.69	1.24	1.24	ERH	7q34		enhancer of rudimentary (Drosophila) homolog

Table 1. Genes and proteins associated with the P311 protein.

HUM31	U30521_at	U30521	PASS	5	6.00	PASS	7	5	4.86	1.24	1.23	1.24	P311	P311 protein	P311 protein
K244_TCEA	D87685_at	D87685	PASS	8	5.63	PASS	9	8	4.56	1.23	1.23	1.23	KIAA0244		similar to human transcription factor TFIIS (S34159).
PSM1131	D88378_at	D88378	PASS	6	6.00	PASS	8	6	4.88	1.23	1.23	1.23		proteasome inhibitor hP131	
SRI	M32886_at	M32886	PASS	8	7.00	PASS	13	8	5.69	1.23	1.23	1.23	SRI	sorcin	sorcin
PRKAR1A	M33336_at	M33336	PASS	7	25.71	PASS	13	7	20.92	1.23	1.23	1.23	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)
AMD1	M21154_at	M21154	PASS	8	8.50	PASS	12	8	6.92	1.23	1.23	1.23	AMD1	S-adenosylmethionine decarboxylase 1	S-adenosylmethionine decarboxylase 1
HG884-HT8	HG884-HT8	HG884-HT8	PASS	5	6.00	PASS	9	5	4.89	1.23	1.23	1.23			
RAB5IP	S83364_at	S83364	PASS	7	11.86	PASS	12	7	9.67	1.23	1.23	1.23	putative Rab5-interacting protein		This sequence comes from Fig. 4.
K35_NOPPI	D21262_at	D21262	PASS	9	7.11	PASS	10	9	5.80	1.23	1.23	1.23	P130	nucleolar phosphoprotein p130	nucleolar phosphoprotein p130
CD36	Z32765_at	Z32765	PASS	8	26.88	PASS	13	8	21.92	1.23	1.23	1.23			
ETFA	J04058_at	J04058	PASS	7	6.57	PASS	11	7	5.36	1.23	1.23	1.23	ETFA	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)
TCEA1	M81601_at	M81601	PASS	8	18.75	PASS	13	8	15.31	1.22	1.22	1.22	transcription elongation factor SII		
GSN	S65738_at	S65738	PASS	9	10.00	PASS	12	9	8.17	1.22	1.22	1.22	actin depolymerizing factor, zing factor, destrin, ADF	actin depolymerizing factor	This sequence comes from Fig. 1B; destrin; ADF
D78132_s_at	D78132_s_at	D78132	PASS	8	7.63	PASS	13	8	6.23	1.22	1.22	1.22	Rheb	ras-related GTP-binding protein	Ras homologue enriched in brain; similar to rat Rheb gene
ITPR2	D26070_at	D26070	PASS	5	5.80	PASS	12	5	4.75	1.22	1.22	1.22	ITPR1	human type 1 inositol 1,4,5-trisphosphate receptor	inositol 1,4,5-trisphosphate receptor, type 1
HG210-HT2	HG210-HT2	HG210-HT2	PASS	5	5.80	PASS	8	5	4.75	1.22	1.22	1.22			
U28488_s_at	U28488_s_at	U28488	PASS	5	7.20	PASS	10	5	5.90	1.22	1.22	1.22	C3AR1	complement component 3a receptor 1	complement component 3a receptor 1
EGR1	S81439_at	S81439	PASS	7	5.86	PASS	10	7	4.80	1.22	1.22	1.22	TIEG		TGFB inducible early growth response
TSC22	U35048_at	U35048	PASS	9	15.11	PASS	13	9	12.38	1.22	1.22	1.22	TSC22	TSC-22 protein	transforming growth factor beta-stimulated protein TSC-22
DCN	M14219_at	M14219	PASS	7	7.43	PASS	11	7	6.09	1.22	1.22	1.22	DCN	decorin	decorin
U00947_s_at	U00947_s_at	U00947	PASS	9	88.89	PASS	13	9	72.92	1.22	1.22	1.22			
K155_COSB	D63875_at	D63875	PASS	8	7.88	PASS	13	8	6.46	1.22	1.22	1.22	KIAA0155		KIAA0155 gene product
X57152_mal	X57152_mal	X57152	PASS	9	28.00	PASS	13	9	23.00	1.22	1.22	1.22		casein kinase II subunit beta	protein kinase
Y00451_s_at	Y00451_s_at	Y00451	PASS	8	5.75	PASS	11	8	4.73	1.22	1.22	1.22	ALAS2	aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)	aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)

HADHB	D16481_at	D16481	PASS	6	9.17	PASS	13	6	7.54	1.22	1.22	HADHB	2p23	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit
PCSK4	HG4297-HT4	HG4297-HT4	PASS	9	24.00	PASS	13	9	19.77	1.21	1.21	ATM	11q22-q23	ataxia telangiectasia mutated (includes complementation groups A, C and D)	ataxia telangiectasia mutated (includes complementation groups A, C and D)
ATM	U33841_at	U33841	PASS	5	6.20	PASS	9	5	5.11	1.21	1.21	ATM	11q22-q23	ataxia telangiectasia mutated (includes complementation groups A, C and D)	ataxia telangiectasia mutated (includes complementation groups A, C and D)
RPL31	X15940_at	X15940	PASS	9	354.56	PASS	13	9	292.46	1.21	1.21	RPL31	2	ribosomal protein L31	ribosomal protein L31
BTK ma3	U78027_ma3	U78027	PASS	9	174.44	PASS	13	9	144.08	1.21	1.21	FTP3		lysosomal exoglycosidase	lysosomal exoglycosidase
X15729_s_at	X15729_s_at	X15729	PASS	9	36.56	PASS	13	9	30.23	1.21	1.21	DDX5	17q21	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD)	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD)
DNAPKCS	U47077_at	U47077	PASS	7	5.29	PASS	8	7	4.38	1.21	1.21	PRKDC	8q11	DNA-dependent protein kinase catalytic subunit	protein kinase, DNA-activated, catalytic polypeptide
CUL3	U58089_at	U58089	PASS	8	9.75	PASS	13	8	8.08	1.21	1.21	CUL3	Chr.2	cullin 3	cullin 3
D28473 s_at	D28473 s_at	D28473	PASS	6	6.33	PASS	12	6	5.25	1.21	1.21	IARS	9q21	isoleucine-tRNA synthetase	isoleucine-tRNA synthetase
J04029_s_at	J04029_s_at	J04029	PASS	9	9.56	PASS	13	9	7.92	1.21	1.21	KRT10	17q21-q23	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)
CDC16HS	U18291_at	U18291	PASS	6	6.83	PASS	12	6	5.67	1.21	1.21	CDC16		cell division cycle 16; anaphase promoting complex 6	cell division cycle 16; anaphase promoting complex 6
HSPE1	U07550_at	U07550	PASS	7	7.43	PASS	11	7	6.18	1.20	1.20	HSPE1		heat shock 10kD protein 1 (chaperonin 10)	heat shock 10kD protein 1 (chaperonin 10)
BTF3 f	HG1515-HT	HG1515-HT	PASS	9	63.44	PASS	13	9	52.85	1.20	1.20				
CD86	U04343_at	U04343	PASS	8	6.00	PASS	9	8	5.00	1.20	1.20	CD86		CD86 antigen	common synonyms are B7-2 and B70; B70 antigen; B7-2
K11	D13636_at	D13636	PASS	6	7.50	PASS	8	6	6.25	1.20	1.20	GTF3C2	2	general transcription factor IIIC, polypeptide 2 (beta subunit, 110kD)	general transcription factor IIIC, polypeptide 2 (beta subunit, 110kD)
SEMAE	AB000220_a	AB000220	PASS	5	6.00	PASS	8	5	5.00	1.20	1.20			senaphloirin E	
TRANSP1	D87127_at	D87127	PASS	5	6.60	PASS	8	5	5.50	1.20	1.20	TLOC1		translocation protein 1	translocation protein 1
X75755_ma1	X75755_ma1	X75755	PASS	7	6.43	PASS	11	7	5.36	1.20	1.20	SFRS2	17	splicing factor, arginine/serine-rich 2	splicing factor, arginine/serine-rich 2
PTPN4	M68941_at	M68941	PASS	7	7.86	PASS	9	7	6.56	1.20	1.20	PTPN4		protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)
TAF2G	U21858_at	U21858	PASS	8	7.00	PASS	13	8	5.85	1.20	1.20	TAF2G		TATA box binding protein (TBP)-associated factor, RNA polymerase II, G, 32kD	TATA box binding protein (TBP)-associated factor, RNA polymerase II, G, 32kD
PIGB	D42138_at	D42138	PASS	6	5.83	PASS	8	6	4.88	1.20	1.20	PIGB	15q21-q22	phosphatidylinositol glycan, class B	phosphatidylinositol glycan, class B
U50527 s_at	U50527 s_at	U50527	PASS	6	5.67	PASS	8	6	4.75	1.19	1.19				
PYGL	M14636_at	M14636	PASS	7	5.71	PASS	10	7	4.80	1.19	1.19	PYGL	14q11.2-q24.3	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)
PSMZ	D38048_at	D38048	PASS	9	10.89	PASS	13	9	9.15	1.19	1.19	PSMB7	9q34.11-q34.12	proteasome (prosome, macropain) subunit, beta type, 7	proteasome (prosome, macropain) subunit, beta type, 7
CASP4	U28014_at	U28014	PASS	9	23.33	PASS	13	9	19.62	1.19	1.19	CASP4	11q22.2-q22.3	caspase 4, apoptosis-related cysteine protease	caspase 4, apoptosis-related cysteine protease

IGFBP7	HG987-HT98	HG987-HT	PASS	7	8.14	PASS	13	7	6.85	1.19	1.19	1.19						
P23	L24804_at	L24804	PASS	5	11.00	PASS	12	5	9.25	1.19	1.19	1.19	p23	3p21.1-p14.2	pyruvate dehydrogenase (lipoamide) beta	pyruvate dehydrogenase (lipoamide) beta		
PDHB	D90086_at	D90086	PASS	9	16.56	PASS	13	9	13.92	1.19	1.19	1.19	PDHB		enterocyte differentiation associated factor EDAF-1	enterocyte differentiation associated factor EDAF-1		
ENTDPPF	U62136_at	U62136	PASS	6	7.00	PASS	9	6	5.89	1.19	1.19	1.19			golgi autoantigen, golgin subfamily a, 4	golgi autoantigen, golgin subfamily a, 4		
TRGGP230	U41740_at	U41740	PASS	6	6.33	PASS	9	6	5.33	1.19	1.19	1.19	GOLGA4	6p22-p12	phosphodiesterase 4B, cAMP-specific (dunce (Drosophila))-homolog phosphodiesterase	phosphodiesterase 4B, cAMP-specific (dunce (Drosophila))-homolog phosphodiesterase		
PDE4B	L20971_at	L20971	PASS	7	6.29	PASS	10	7	5.30	1.19	1.19	1.19	PDE4B	1p31	phosphodiesterase 4B, cAMP-specific (dunce (Drosophila))-homolog phosphodiesterase	phosphodiesterase 4B, cAMP-specific (dunce (Drosophila))-homolog phosphodiesterase		
MLH1	U07418_at	U07418	PASS	9	7.11	PASS	12	9	6.00	1.19	1.19	1.19	hmlh1		human homolog of E. coli mutL gene product, Swiss-Prot Accession Number P23367	human homolog of E. coli mutL gene product, Swiss-Prot Accession Number P23367		
CTNNA1	U03100_at	U03100	PASS	5	6.40	PASS	10	5	5.40	1.19	1.19	1.19	CTNNA1	5q31	catenin (cadherin-associated protein), alpha 1 (102kD)	catenin (cadherin-associated protein), alpha 1 (102kD)		
BAP	U72511_at	U72511	PASS	9	29.78	PASS	13	9	25.15	1.18	1.18	1.18	hBAP		BAP; prohibitin related protein; similar to EST with GenBank Accession Number H45225; see corresponding genomic sequence in GenBank Accession Number U72506	BAP; prohibitin related protein; similar to EST with GenBank Accession Number H45225; see corresponding genomic sequence in GenBank Accession Number U72506		
PSMA2	M64992_at	M64992	PASS	9	14.11	PASS	13	9	11.92	1.18	1.18	1.18	PSMA1	11p15.1	proteasome (prosome, macropain) subunit, alpha type, 1	proteasome (prosome, macropain) subunit, alpha type, 1		
HINT	U51004_at	U51004	PASS	9	49.89	PASS	13	9	42.15	1.18	1.18	1.18	PKC1-1		protein kinase C inhibitor	protein kinase C inhibitor		
MPP11	X98260_at	X98260	PASS	5	7.00	PASS	12	5	5.92	1.18	1.18	1.18	mpp11		M-phase phosphoprotein 11	M-phase phosphoprotein 11		
PAM	M37721_at	M37721	PASS	9	5.56	PASS	10	9	4.70	1.18	1.18	1.18	PAM	5q	peptidylglycine alpha-amidating monooxygenase	peptidylglycine alpha-amidating monooxygenase		
K143_COSCE	D63477_at	D63477	PASS	8	6.00	PASS	13	8	5.08	1.18	1.18	1.18	K1AA0143		The K1AA0143 gene product is related to a putative C.elegans gene encoded on cosmid C32D5.	The K1AA0143 gene product is related to a putative C.elegans gene encoded on cosmid C32D5.		
BRG1	U29175_at	U29175	PASS	9	7.78	PASS	12	9	6.58	1.18	1.18	1.18	BRG1		transcriptional activator	transcriptional activator		
H2B f	M60750 f at	M60750	PASS	7	10.71	PASS	13	7	9.08	1.18	1.18	1.18	H2BFL	6p21.3	H2B histone family, member L	H2B histone family, member L		
SAS	U01160_at	U01160	PASS	9	5.56	PASS	7	9	4.71	1.18	1.18	1.18	SAS		SAS	SAS		
TP53BP2	U50078_at	U50078	PASS	7	8.14	PASS	13	7	6.92	1.18	1.18	1.18	HERC1	15qter-pter	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1		
CRE5	AFFX-CreX	AFFX-CreX	PASS	9	199.44	PASS	13	9	170.00	1.17	1.17	1.17						
GRL	M10901 at	M10901	PASS	8	7.13	PASS	13	8	6.08	1.17	1.17	1.17	GRL	5q31-q32	glucocorticoid receptor	glucocorticoid receptor		
PGE2R	U19487 at	U19487	PASS	5	5.60	PASS	9	5	4.78	1.17	1.17	1.17	PTGER2	5p13.1	prostaglandin E receptor 2 (subtype EP2), 53kD	prostaglandin E receptor 2 (subtype EP2), 53kD		
DNAJ	L08069 at	L08069	PASS	8	11.63	PASS	13	8	9.92	1.17	1.17	1.17	HSJ2		heat shock protein, DNAJ-like 2	heat shock protein, DNAJ-like 2		
HG2815-HT2	HG2815-HT2	HG2815-H	PASS	9	37.67	PASS	13	9	32.15	1.17	1.17	1.17						
GAPDH5	AFFX-HUM6	AFFX-HUN	PASS	9	124.78	PASS	13	9	106.54	1.17	1.17	1.17						
U30827_s_at	U30827_s_at	U30827	PASS	9	21.33	PASS	13	9	18.23	1.17	1.17	1.17	SRp40		member of the family of SR protein pre-mRNA splicing factors; alternatively spliced	member of the family of SR protein pre-mRNA splicing factors; alternatively spliced		

ERP31	X94910_at	X94910	PASS	8	19.25	PASS	13	8	16.46	1.17	1.17		ERp28	Similar to ULA_5 product, AC P30040
TCP1	X52882_at	X52882	PASS	8	11.38	PASS	12	8	9.75	1.17	1.17			t-complex polypeptide 1 (AA 1-556)
DAP5	AFFX-DapX	AFFX-DapX	PASS	9	242.44	PASS	13	9	207.85	1.17	1.17			
SGTPBP	U57094_at	U57094	PASS	6	11.00	PASS	9	6	9.44	1.16	1.16		RAB27A, member RAS oncogene family	RAB27A, member RAS oncogene family
SF2P32	M69039_at	M69039	PASS	8	9.13	PASS	13	8	7.85	1.16	1.16		complement component 1, q subcomponent binding protein	complement component 1, q subcomponent binding protein
UBE2A	M74524_at	M74524	PASS	7	6.00	PASS	12	7	5.17	1.16	1.16		ubiquitin-conjugating enzyme E2A (RAD6 homolog)	ubiquitin-conjugating enzyme E2A (RAD6 homolog)
CCT4	U38846_at	U38846	PASS	9	30.67	PASS	13	9	26.46	1.16	1.16		stimulator of TAR RNA binding	stimulator of TAR RNA binding
FRG1	L76159_at	L76159	PASS	6	7.67	PASS	13	6	6.62	1.16	1.16		FSHD region gene 1	FSHD region gene 1
M57466_s_at	M57466_s_at	M57466	PASS	9	70.67	PASS	13	9	61.08	1.16	1.16		major histocompatibility complex, class II, DP beta 1	major histocompatibility complex, class II, DP beta 1
U44799_s_at	U44799_s_at	U44799	PASS	6	6.00	PASS	10	6	5.20	1.15	1.15		U1-snRNP binding protein homolog	U1-snRNP binding protein homolog
RASA1	M23379_at	M23379	PASS	5	6.00	PASS	10	5	5.20	1.15	1.15		RAS p21 protein activator (GTPase activating protein) 1	RAS p21 protein activator (GTPase activating protein) 1
J02621_s_at	J02621_s_at	J02621	PASS	9	26.44	PASS	13	9	22.92	1.15	1.15			high-mobility group (nonhistone chromosomal) protein 14
YES1	M15990_at	M15990	PASS	7	5.43	PASS	7	7	4.71	1.15	1.15			v-src-1 Yamaguchi sarcoma viral oncogene homolog 1
CTSL	X12451_at	X12451	PASS	6	6.33	PASS	10	6	5.50	1.15	1.15		cathepsin L	cathepsin L
W19119	M24069_at	M24069	PASS	7	6.71	PASS	12	7	5.83	1.15	1.15		cold shock domain protein A	cold shock domain protein A
Z25521_s_at	Z25521_s_at	Z25521	PASS	9	16.11	PASS	13	9	14.00	1.15	1.15		integrin associated protein	integrin associated protein
CISACTS	M82882_at	M82882	PASS	7	7.86	PASS	12	7	6.83	1.15	1.15			E74-like factor 1 (ets domain transcription factor)
K181	D80003_at	D80003	PASS	8	6.13	PASS	12	8	5.33	1.15	1.15			
CAMLG	U18242_at	U18242	PASS	7	6.57	PASS	11	7	5.73	1.15	1.15		calcium modulating ligand	calcium modulating ligand
RANBP1	D38076_at	D38076	PASS	7	9.00	PASS	13	7	7.85	1.15	1.15		RAN binding protein 1	RAN binding protein 1
ICT1	X81788_at	X81788	PASS	7	6.14	PASS	11	7	5.36	1.15	1.15		immature colon carcinoma transcript 1	immature colon carcinoma transcript 1
RB1	L41870_at	L41870	PASS	7	5.86	PASS	8	7	5.13	1.14	1.14		retinoblastoma 1 (including osteosarcoma)	retinoblastoma 1 (including osteosarcoma)
K254	D87443_at	D87443	PASS	7	4.57	PASS	7	7	4.00	1.14	1.14		KIAA0254 gene product	KIAA0254 gene product
HG1428-HT	HG1428-HT	HG1428-HT	PASS	9	286.67	PASS	13	9	250.92	1.14	1.14			
M31520_ma	M31520_ma	M31520	PASS	9	154.78	PASS	13	9	135.54	1.14	1.14		ribosomal protein S24	ribosomal protein S24
NAP1L1	M86667_at	M86667	PASS	9	33.78	PASS	13	9	29.62	1.14	1.14		nucleosome assembly protein 1-like 1	nucleosome assembly protein 1-like 1
RBM3	U28686_at	U28686	PASS	8	12.13	PASS	11	8	10.64	1.14	1.14		RNA binding motif protein 3	RNA binding motif protein 3
U58046_s_at	U58046_s_at	U58046	PASS	5	5.80	PASS	10	5	5.10	1.14	1.14		eukaryotic translation initiation factor 3, subunit 10 (theta, 170kD)	eukaryotic translation initiation factor 3, subunit 10 (theta, 170kD)
VBPI	U56833_at	U56833	PASS	8	6.38	PASS	13	8	5.62	1.14	1.14		von Hippel-Lindau binding protein 1	von Hippel-Lindau binding protein 1
TCLLYM	X82240_ma	X82240	PASS	5	15.20	PASS	12	5	13.42	1.13	1.13		T-cell leukemia/lymphoma 1A	T-cell leukemia/lymphoma 1A
ACPI	U25849_at	U25849	PASS	6	9.83	PASS	13	6	8.69	1.13	1.13		acid phosphatase 1, soluble	acid phosphatase 1, soluble
M60483_ma	M60483_ma	M60483	PASS	8	6.50	PASS	12	8	5.75	1.13	1.13		protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform

PSMHC8	D00762_at	D00762	PASS	7	11.43	PASS	9	7	10.11	1.13	1.13	PSMA3	14q23	proteasome (prosome, macropain) subunit, alpha type, 3	proteasome (prosome, macropain) subunit, alpha type, 3
LGALS2	M87860_at	M87860	PASS	7	26.71	PASS	11	7	23.64	1.13	1.13	LGALS2		S-lac lectin	
D11327_s_at	D11327_s_at	D11327	PASS	8	5.75	PASS	10	8	5.10	1.13	1.13	PTPN7	1q32.1	protein tyrosine phosphatase, non-receptor type 7	protein tyrosine phosphatase, non-receptor type 7
EFS3	L34587_at	L34587	PASS	9	13.78	PASS	13	9	12.23	1.13	1.13			RNA polymerase II elongation factor SIII, p15 subunit	putative
FEZ2	U60061_at	U60061	PASS	6	5.83	PASS	11	6	5.18	1.13	1.13	FEZ2		FEZ2	zygyn 2
U49020_cds3	U49020_cds3	U49020	PASS	8	5.75	PASS	9	8	5.11	1.13	1.13	MEF2A		myocyte-specific enhancer factor 2A, C4 form	
PPM1A	S87759_at	S87759	PASS	7	6.00	PASS	9	7	5.33	1.13	1.13	PPM1B		protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform
EIF4A2	D30655_at	D30655	PASS	9	60.56	PASS	13	9	53.85	1.12	1.12	EIF4A2	18p11.2	eukaryotic translation initiation factor 4A, isoform 2	eukaryotic translation initiation factor 4A, isoform 2
GRLB	HG4582-HT4	HG4582-H	PASS	5	5.60	PASS	11	5	5.00	1.12	1.12			thiopurine methyltransferase	35 kDa monomer; cytosolic protein
U12387_s_at	U12387_s_at	U12387	PASS	5	6.60	PASS	10	5	5.90	1.12	1.12	TPMT		C-Type lectin	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)
AICL	X96719_at	X96719	PASS	5	18.40	PASS	13	5	16.46	1.12	1.12	CLECSF2	12p		
K69_DS0556	D31885_at	D31885	PASS	9	16.56	PASS	13	9	14.85	1.12	1.12	KIAA0069			
PSMA5	X61970_at	X61970	PASS	9	13.11	PASS	13	9	11.77	1.11	1.11	PSMA5	1p13	proteasome (prosome, macropain) subunit, alpha type, 5	proteasome (prosome, macropain) subunit, alpha type, 5
PRPS1	D00860_at	D00860	PASS	9	6.11	PASS	12	9	5.50	1.11	1.11	PRPS1	Xq21-q27	phosphoribosyl pyrophosphate synthetase 1	phosphoribosyl pyrophosphate synthetase 1
U33936_s_at	U33936_s_at	U33936	PASS	7	5.86	PASS	11	7	5.27	1.11	1.11	ADK	10cen-q24	adenosine kinase	adenosine kinase
LCP2	U20158_at	U20158	PASS	9	17.00	PASS	13	9	15.31	1.11	1.11	SLP-76		76 kDa tyrosine phosphoprotein	76 kDa tyrosine phosphoprotein
HG2981-HT	HG2981-HT	HG2981-H	PASS	7	10.29	PASS	11	7	9.27	1.11	1.11				
PPIB	M63573_at	M63573	PASS	7	17.29	PASS	12	7	15.58	1.11	1.11	PPIB	15	peptidylprolyl isomerase B (cyclophilin B)	peptidylprolyl isomerase B (cyclophilin B)
B56E	L76703_at	L76703	PASS	6	5.17	PASS	9	6	4.67	1.11	1.11	PPP2R5E	7p11.2-p12	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform
E_23801	U79282_at	U79282	PASS	5	5.20	PASS	10	5	4.70	1.11	1.11				
HSPA8	HG2855-HT	HG2855-H	PASS	9	38.56	PASS	13	9	35.00	1.10	1.10				
H2AZ	M37583_at	M37583	PASS	9	18.11	PASS	13	9	16.46	1.10	1.10	H2AFZ	4q24	H2A histone family, member Z	H2A histone family, member Z
PHC11	J04973_at	J04973	PASS	9	12.78	PASS	13	9	11.62	1.10	1.10	UQCRC2	16p12	ubiquinol-cytochrome c reductase core protein II	ubiquinol-cytochrome c reductase core protein II
TCRD	M21624_at	M21624	PASS	9	17.33	PASS	13	9	15.77	1.10	1.10	TCRD	14q11.2	T-cell receptor, delta (V.D.J.C)	T-cell receptor, delta (V.D.J.C)
TNFAIP3	M59465_at	M59465	PASS	9	13.33	PASS	13	9	12.15	1.10	1.10	TNFAIP1	17q22-q23	tumor necrosis factor, alpha-induced protein 1 (endothelial)	tumor necrosis factor, alpha-induced protein 1 (endothelial)
APBB1	U50939_at	U50939	PASS	7	6.57	PASS	12	7	6.00	1.10	1.10	APPBP1	16q22	Amyloid beta precursor protein-binding protein 1	amyloid beta precursor protein-binding protein 1, 59kD
BACTINM	AFFX-HSAC	AFFX-HSA	PASS	9	330.67	PASS	13	9	302.92	1.09	1.09				
D13S824E	U47635_at	U47635	PASS	6	6.67	PASS	9	6	6.11	1.09	1.09			DSEG number: D13S824E; orf	
RAD23B	D21090_at	D21090	PASS	7	6.00	PASS	12	7	5.50	1.09	1.09	RAD23B	3p25.1	RAD23 (S. cerevisiae) homolog B	RAD23 (S. cerevisiae) homolog B

PSMD4	U24704_at	U24704	PASS	7	11.29	PASS	11	7	10.36	1.09	1.09	antiseretory factor-1	similar to Human S5a proteasome subunit, Genbank Accession Number U51007	
PRKMK1	L11284_at	L11284	PASS	7	10.29	PASS	13	7	9.46	1.09	1.09	PRKMK1	15q22.1-q22.33	protein kinase, mitogen-activated, kinase 1 (MAP kinase kinase 1)
BIOB5	AFFX-BioB-	AFFX-BioB-	PASS	9	113.56	PASS	13	9	104.69	1.08	1.08			DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophysin)
LKP	L13848_at	L13848	PASS	6	10.83	PASS	10	6	10.00	1.08	1.08	DDX9	1q25	elongation factor Ts
EFTS	L37936_at	L37936	PASS	8	10.38	PASS	12	8	9.58	1.08	1.08			heterochromatin protein p25
CBX	U35451_at	U35451	PASS	6	6.17	PASS	10	6	5.70	1.08	1.08	p25beta		basic transcription factor 2 p44
SMN1_ma3	U80017_ma3	U80017	PASS	7	6.00	PASS	9	7	5.56	1.08	1.08	btf2p44		eukaryotic translation elongation factor 1 alpha 2
X03689_s_at	X03689_s_at	X03689	PASS	9	224.56	PASS	13	9	208.08	1.08	1.08	EEF1A2	20q13.3	phosphoribosyl pyrophosphate synthetase 2
PRPS2	Y00971_at	Y00971	PASS	5	5.00	PASS	11	5	4.64	1.08	1.08	PRPS2	Xpter-q21	ATP synthase gamma-subunit
ATP5C1	D16562_at	D16562	PASS	9	29.67	PASS	13	9	27.54	1.08	1.08			The KIAA0191 gene is expressed ubiquitously.; The KIAA0191 protein retains the C2H2 zinc-finger at its N-terminal region.
K191	D83776_at	D83776	PASS	5	6.00	PASS	7	5	5.57	1.08	1.08	KIAA0191		fragile X mental retardation 1
M67468_s_at	M67468_s_at	M67468	PASS	7	5.14	PASS	9	7	4.78	1.08	1.08	FMR1	Xq27.3	annexin VII (synexin)
ANX7	J04543_at	J04543	PASS	8	8.25	PASS	12	8	7.67	1.08	1.08	ANX7	10q21.1-q21.2	EBI 2: EBV induced G-protein-coupled receptor
CMKBR7	L08177_at	L08177	PASS	8	5.38	PASS	10	8	5.00	1.08	1.08	EBI2	13	Similar to N-terminal regions of diazotroph NifU proteins
NIFUL	U47101_at	U47101	PASS	9	26.78	PASS	13	9	24.92	1.07	1.07	hNifU		similar to a C.elegans ZK353.8 protein (S44655)
K242_HYP5	D87684_at	D87684	PASS	8	8.13	PASS	10	8	7.60	1.07	1.07	KIAA0242		lymphocyte cytosolic protein 1 (L-plasin)
LCP1	J02923_at	J02923	PASS	9	45.67	PASS	13	9	42.77	1.07	1.07	LCP1	13q14.3	ORF; putative
S203_15	L40395_at	L40395	PASS	8	6.50	PASS	9	8	6.11	1.06	1.06			pre-B-cell leukemia transcription factor 3
LAML	HG1078-HT	HG1078-H	PASS	7	13.00	PASS	13	7	12.23	1.06	1.06			signal recognition particle 9kD
PBX3	X59841_at	X59841	PASS	6	5.67	PASS	9	6	5.33	1.06	1.06	PBX3	9q33-q34	signal transducer CD24
SRP9	U20998_at	U20998	PASS	9	15.44	PASS	13	9	14.54	1.06	1.06	SRP9		cell growth regulator CGR19
L33930_s_at	L33930_s_at	L33930	PASS	6	4.67	PASS	10	6	4.40	1.06	1.06			SFRS protein kinase 2
CGR19	U66469_at	U66469	PASS	5	5.40	PASS	10	5	5.10	1.06	1.06			beta-2-microglobulin
SRPK2	U88666_at	U88666	PASS	8	5.38	PASS	12	8	5.08	1.06	1.06	SRPK2	7q22-q31.1	signal recognition particle 54kD
B2M	S82297_at	S82297	PASS	9	164.00	PASS	13	9	155.15	1.06	1.06	B2M	15q21-q22.2	amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)
SRP54	U51920_at	U51920	PASS	6	5.17	PASS	10	6	4.90	1.05	1.05	SRP54		
U84011_s_at	U84011_s_at	U84011	PASS	5	4.80	PASS	9	5	4.56	1.05	1.05	AGL	1p21	
E_23865	U90912_at	U90912	PASS	7	5.71	PASS	7	7	5.43	1.05	1.05			splicing factor, arginine/serine-rich 9
SFRS3	U30825_at	U30825	PASS	9	31.44	PASS	13	9	29.92	1.05	1.05	SFRS9		

HNRPH2	U01923_at	U01923	PASS	7	6.71	PASS	10	7	6.40	1.05	1.05					
RPL14	D87735_at	D87735	PASS	9	150.33	PASS	13	9	143.31	1.05	1.05	RPL14			ribosomal protein L14	
W52B_f	HG3576-HT	HG3576-HT	PASS	9	106.89	PASS	13	9	102.08	1.05	1.05					
AMFR	M63175_at	M63175	PASS	5	6.80	PASS	8	5	6.50	1.05	1.05	AMFR	16q21		autocrine motility factor receptor	
K73_CYCRP	D38552_at	D38552	PASS	6	6.83	PASS	13	6	6.54	1.05	1.05	K1AA0073			The hsl539 protein is related to cyclophilin.	
MCM3	D38073_at	D38073	PASS	8	6.88	PASS	10	8	6.60	1.04	1.04	MCM3	6p12		minichromosome maintenance deficient (S. cerevisiae) 3	
PAK3	U25975_at	U25975	PASS	5	5.60	PASS	10	5	5.40	1.04	1.04	hPAK65			macCDC42Hs activated kinase; serine kinase; Method: conceptual translation supplied by author	
U67122_s_at	U67122_s_at	U67122	PASS	7	11.00	PASS	13	7	10.62	1.04	1.04				SUMO-1	conjugated post-translationally to RanGAP1; ubiquitin-related protein; similar to UBL1 encoded by GenBank Accession Number U38784, PIC1 encoded by GenBank Accession Number U61397 and GMP1 encoded by GenBank Accession Number U72722
L06797_s_at	L06797_s_at	L06797	PASS	9	33.67	PASS	13	9	32.54	1.03	1.03	CXCR4	2q21		Neuropeptide Y receptor Y3	chemokine (C-X-C motif), receptor 4 (fusin)
CAT_ma1	X04085_ma1	X04085	PASS	7	15.43	PASS	13	7	14.92	1.03	1.03				catalase	
SFRS3	D28423_at	D28423	PASS	6	17.33	PASS	12	6	16.83	1.03	1.03				pre-miRNA splicing factor SRp20	
J02683_s_at	J02683_s_at	J02683	PASS	9	31.56	PASS	13	9	30.69	1.03	1.03	ANT2	Xq24-q26		adenine nucleotide translocator 2 (fibroblast)	adenine nucleotide translocator 2 (fibroblast)
RPS7_ma1	Z25749_ma1	Z25749	PASS	9	136.56	PASS	13	9	132.85	1.03	1.03	RPS7	2p25		ribosomal protein S7	
HDAC2	U31814_at	U31814	PASS	9	6.78	PASS	10	9	6.60	1.03	1.03	HDAC2	6q21		histone deacetylase 2	
M60974_s_at	M60974_s_at	M60974	PASS	5	5.60	PASS	10	5	5.50	1.02	1.02	DDIT1	1p34-p12		DNA-damage-inducible transcript 1	DNA-damage-inducible transcript 1
SEMA	U60800_at	U60800	PASS	9	22.22	PASS	13	9	21.85	1.02	1.02	CD100			semaphorin	
D13631_s_at	D13631_s_at	D13631	PASS	7	11.00	PASS	12	7	10.83	1.02	1.02	KIAA0006				
PRKACB	M34181_at	M34181	PASS	5	6.80	PASS	10	5	6.70	1.01	1.01	PRKACB	1		protein kinase, cAMP-dependent, catalytic, beta	protein kinase, cAMP-dependent, catalytic, beta
M26730_s_at	M26730_s_at	M26730	PASS	9	33.78	PASS	13	9	33.31	1.01	1.01	UQB			ubiquitin-binding protein (QP)	ubiquitin-binding protein (QP)
GDI2	D13988_at	D13988	PASS	6	18.17	PASS	13	6	18.00	1.01	1.01	GDI2	10p15		GDP dissociation inhibitor 2	GDP dissociation inhibitor 2
RPL44	M15661_at	M15661	PASS	9	51.44	PASS	13	9	51.08	1.01	1.01	RPL44			ribosomal protein L44	ribosomal protein L44
ZFPRES24	AB000468_at	AB000468	PASS	8	18.75	PASS	13	8	18.69	1.00	1.00	RNF4	4p16.3		ring finger protein 4	ring finger protein 4
BACTIN5	AFFX-HSAC	AFFX-HSAC	PASS	9	240.44	PASS	13	9	240.00	1.00	1.00					
M87507_s_at	M87507_s_at	M87507	PASS	6	7.50	PASS	12	6	7.50	1.00	1.00	CASP1	11q23		caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)
UVRAG_ma1	X99050_ma1	X99050	PASS	6	5.00	PASS	11	6	5.00	1.00	1.00	UVRAG	11q13		UV radiation resistance associated gene	UV radiation resistance associated gene
RP3	U02556_at	U02556	PASS	5	6.00	PASS	12	5	6.00	1.00	1.00				70kDa peroxisomal membrane protein	RP3 candidate gene
X58528_s_at	X58528_s_at	X58528	PASS	5	5.20	PASS	10	5	5.20	1.00	1.00	PMP70				
SFRS3	L10838_at	L10838	PASS	8	17.13	PASS	13	8	17.23	-1.01	-1.01	SFRS3			splicing factor, arginine/serine-rich 3	splicing factor, arginine/serine-rich 3
METPEP	U29607_at	U29607	PASS	9	27.22	PASS	13	9	27.69	0.98	-1.02				methionine aminopeptidase	

K253	D87442_at	D87442	PASS	6	8.17	PASS	9	6	8.33	0.98	-1.02	KIAA0253			
CRE3	AFFX-CreX-AFFX-CreX	PASS	9	27.78	PASS	13	9	28.46	0.98	-1.02					
UBE2D3	U39318_at	U39318	PASS	8	19.00	PASS	13	8	19.54	0.97	-1.03	UBCH5C	UbcH5C	Transcript is widely expressed. Related to S. Cerevisiae UBC4 and UBC5. Closely related to human UbcH5(A) and to UbcH5B	
U26312_s_at	U26312_s_at	U26312	PASS	6	5.67	PASS	12	6	5.83	0.97	-1.03		HP1Hs-gamma	similar to Drosophila heterochromatin protein HP1 Swiss Prot Accession Number P29227, and to human heterochromatin protein HP1Hs-alpha encoded by GenBank Accession Number U26311; contains chromo domain; recognized by autoantibodies from some patients with scleroderma; heterochromatin protein	
H33B	Z48950_at	Z48950	PASS	9	66.78	PASS	13	9	68.85	0.97	-1.03	H3F3B	histone H3.3	H3 histone, family 3B (H3.3B)	
HNRPF	L28010_at	L28010	PASS	9	14.89	PASS	13	9	15.38	0.97	-1.03	HNRPF	HnRNP F protein	heterogeneous nuclear ribonucleoprotein F	
E 23665	U90913_at	U90913	PASS	7	6.00	PASS	10	7	6.20	0.97	-1.03			Major histocompatibility complex, class II, Y box-binding protein I; DNA-binding protein B	
YB1	J03827_at	J03827	PASS	9	70.00	PASS	13	9	72.38	0.97	-1.03	YB1			
ID2B	M96843_at	M96843	PASS	9	7.33	PASS	13	9	7.62	0.96	-1.04	Id2B	contractile protein		
MGC24	D14043_at	D14043	PASS	9	14.22	PASS	13	9	14.77	0.96	-1.04		MGC-24 precursor		
NDUFB3	X99728_at	X99728	PASS	8	8.63	PASS	13	8	9.00	0.96	-1.04				
MTND1	L04490_at	L04490	PASS	7	5.86	PASS	8	7	6.13	0.96	-1.05	NDUFA9	NADH dehydrogenase (ubiquinone) 12p	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (39kD)	
STATH	U51678_at	U51678	PASS	8	10.88	PASS	13	8	11.38	0.96	-1.05		small acidic protein		
X83416_s_at	X83416_s_at	X83416	PASS	7	6.00	PASS	13	7	6.31	0.95	-1.05	PRNP	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)	
UBE2L1	S81003_at	S81003	PASS	9	14.00	PASS	13	9	14.77	0.95	-1.05	UBE2L3	ubiquitin-conjugating enzyme E2L 3	ubiquitin-conjugating enzyme E2L 3	
EIF2A	J02645_at	J02645	PASS	5	7.80	PASS	8	5	8.25	0.95	-1.06	EIF2A	eukaryotic translation initiation factor 2A	eukaryotic translation initiation factor 2A	
DLD_ma1	L13761_ma1	L13761	PASS	9	6.67	PASS	12	9	7.08	0.94	-1.06	DLD	dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex)	dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex)	
OCLSF	U63717_at	U63717	PASS	7	7.00	PASS	8	7	7.50	0.93	-1.07		osteoclast stimulating factor	OSF; contains SH3 domain and ankyrin repeat	
GNAO1	U01833_at	U01833	PASS	5	5.60	PASS	9	5	6.00	0.93	-1.07	NBP1	nucleotide binding protein 1 (E.coli MinD like)	nucleotide binding protein 1 (E.coli MinD like)	

M63838_s_at	M63838_s_at	M63838	PASS	9	12.33	PASS	13	9	13.23	0.93	-1.07	IFI16	1q12-qter	interferon-gamma induced protein	interferon, gamma-inducible protein 16
ADD3	U37122_at	U37122	PASS	7	20.71	PASS	13	7	22.23	0.93	-1.07	ADD3	10q24.2-q24.3	adducin gamma subunit	adducin 3 (gamma)
MLLT2	L13773_at	L13773	PASS	9	6.00	PASS	12	9	6.50	0.92	-1.08	AF4			
Z69030_s_at	Z69030_s_at	Z69030	PASS	7	12.71	PASS	12	7	13.83	0.92	-1.09			gamma 1 isoform of 61kDa regulatory subunit of PP2A	
TIG1_xpt1	U49973_xpt1	U49973	PASS	9	7.56	PASS	13	9	8.23	0.92	-1.09				ORF1; MER37; putative transposase similar to pogo element
BTKAP135	U77948_at	U77948	PASS	5	8.40	PASS	13	5	9.15	0.92	-1.09	GTF2I	7q11.23	general transcription factor II, i	general transcription factor II, i
HOU	U32849_at	U32849	PASS	9	10.00	PASS	12	9	10.92	0.92	-1.09	NMI	22q13.3	N-myc (and STAT) interactor	N-myc (and STAT) interactor
KLRB1	HG4263-HT4	HG4263-H	PASS	9	14.78	PASS	13	9	16.15	0.91	-1.09				
AHNAK	M80899_at	M80899	PASS	7	18.14	PASS	12	7	19.83	0.91	-1.09	AHNAK	11q12-q13		AHNAK nucleoprotein (desmoyokin)
NA	X80909_at	X80909	PASS	9	129.22	PASS	13	9	142.69	0.91	-1.10	alpha NAC		Nascent polypeptide associated complex alpha subunit	
JAK1	M64174_at	M64174	PASS	5	8.80	PASS	13	5	9.85	0.89	-1.12	JAK1	1p32.3-p31.3	Janus kinase 1 (a protein tyrosine kinase)	Janus kinase 1 (a protein tyrosine kinase)
Z48501_s_at	Z48501_s_at	Z48501	PASS	9	113.67	PASS	13	9	127.77	0.89	-1.12	PABPL1	3q22-q25	poly(A)-binding protein-like 1	poly(A)-binding protein-like 1
PRTKHT31	HG2167-HT2	HG2167-H	PASS	5	7.00	PASS	9	5	7.89	0.89	-1.13				
K192_MOPA	D83783_at	D83783	PASS	6	6.00	PASS	13	6	6.77	0.89	-1.13	TRAP230	Xq13		thyroid hormone receptor-associated protein, 230 kDa subunit
PRF1	M31951_at	M31951	PASS	6	23.33	PASS	12	6	26.67	0.88	-1.14	PRF1	10q22		perforin 1 (preforming protein)
PSMC2	D11094_at	D11094	PASS	7	9.71	PASS	12	7	11.17	0.87	-1.15	PSMC2	7q22.1-q22.3	proteasome (prosome, macropain) 26S subunit, ATPase, 2	proteasome (prosome, macropain) 26S subunit, ATPase, 2
SDHB	U17886_at	U17886	PASS	5	8.00	PASS	12	5	9.25	0.86	-1.16	sdhB		succinate dehydrogenase iron-protein subunit B	
M21119_s_at	M21119_s_at	M21119	PASS	8	59.00	PASS	13	8	69.15	0.85	-1.17				lysozyme precursor (EC 3.2.1.17)
S311125	L40397_at	L40397	PASS	9	10.78	PASS	13	9	12.77	0.84	-1.18				ORF; putative
RNASE6	U64998_at	U64998	PASS	6	13.33	PASS	10	6	15.80	0.84	-1.19			ribonuclease k6 precursor	RNase k6
IK	S74221_at	S74221	PASS	8	10.13	PASS	12	8	12.08	0.84	-1.19	IK	2p15-p14	IK cytokine, down-regulator of HLA II	IK cytokine, down-regulator of HLA II
U73477_s_at	U73477_s_at	U73477	PASS	6	6.00	PASS	10	6	7.20	0.83	-1.20			acidic nuclear phosphoprotein pp32	LANP; PHAPI; I-1pp2a
M97796_s_at	M97796_s_at	M97796	PASS	6	17.83	PASS	13	6	21.62	0.83	-1.21	ID2	2p25	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
NIP2	U15173_at	U15173	PASS	8	4.88	PASS	12	8	5.92	0.82	-1.21	BNIP2		BCL2/adenovirus E1B 19kD-interacting protein 2	BCL2/adenovirus E1B 19kD-interacting protein 2
POLR2B	X63563_at	X63563	PASS	7	6.71	PASS	12	7	8.17	0.82	-1.22	POLR2B	4q12	polymerase (RNA) II (DNA directed) polypeptide B (140kD)	polymerase (RNA) II (DNA directed) polypeptide B (140kD)
AFFX-CreX	AFFX-CreX	AFFX-CreX	PASS	8	15.38	PASS	13	8	18.77	0.82	-1.22				
TRAMP	X63679_at	X63679	PASS	6	8.50	PASS	13	6	10.38	0.82	-1.22	TRAM		TRAM protein	
SAP18	U96915_at	U96915	PASS	8	13.13	PASS	13	8	16.08	0.82	-1.22	SAP18		sin3 associated polypeptide p18	SAP18p
BIOC5	AFFX-BioC	AFFX-BioC	PASS	9	16.00	PASS	13	9	19.62	0.82	-1.23				
RBI	HG4036-HT4	HG4036-H	PASS	8	11.13	PASS	13	8	14.31	0.78	-1.29				
TFA	L06633_at	L06633	PASS	8	6.75	PASS	13	8	8.85	0.76	-1.31	HE	2	cytohesin binding protein HE	cytohesin binding protein HE
IL7R	M29696_at	M29696	PASS	8	26.38	PASS	11	8	34.73	0.76	-1.32	IL7R	5p13	interleukin 7 receptor	interleukin 7 receptor

Cellular Enzymes

ZFP20	HG3454-HT	HG3454-H	PASS	7	5.43	PASS	9	7	7.22	0.75	-1.33				
COPB	X70476_at	X70476	PASS	8	6.38	PASS	13	8	8.92	0.71	-1.40	COPB2	3q23	coatmer protein complex, subunit beta 2 (beta prime)	coatmer protein complex, subunit beta 2 (beta prime)
RAP1B	HG3521-HT	HG3521-H	PASS	9	17.56	PASS	13	9	25.62	0.69	-1.46				
BIOB3	AFFX-BioB	AFFX-BioB	PASS	9	27.11	PASS	13	9	39.77	0.68	-1.47				
PROGBP	Y12711_at	Y12711	PASS	6	9.33	PASS	13	6	14.00	0.67	-1.50			putative progesterone binding protein	
M27394 s a	M27394 s a	M27394	PASS	6	6.00	PASS	11	6	9.73	0.62	-1.62			cell surface antigen B1	
DAP3	AFFX-DapX	AFFX-Dap	PASS	9	6.56	PASS	13	9	10.69	0.61	-1.63				
M14483_ma	M14483_ma	M14483	PASS	9	65.89	PASS	13	9	109.31	0.60	-1.66	PTMA	2	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
BIOD3	AFFX-BioDn	AFFX-BioD	PASS	9	29.56	PASS	13	9	65.62	0.45	-2.22				

Table 2

6800 human RA Phosphatase and Kinase list

6800 human RA Phosphatase and Kinase list

name	qualifier	GeneSpring qualifier	Patients			Normals			Avg Freq Normals	Ratio	Fold Change	Symbol	Chromoso me	Description	Kinase or Phosphatase
			called "p">4	#"p" (RA)	Avg Freq - RA Patients	called "p">6	#"p" (Normal)	#"p" (RA)							
Kinases															
RAC2	M64595_at	M64595	fail	3		PASS	13	3	19.85	Normal	Normal	RAC2	22q12-q13.2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	Kinase
FRAP	L34075_at	L34075	fail	1		PASS	11	1	5.73	Normal	Normal	FRAP1	1p36.2	FKBP-rapamycin associated protein	Kinase
CAMKA2	U81554_at	U81554	fail	1		PASS	10	1	5.50	Normal	Normal	CAMK2G	10q22	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	Kinase
CDK7	L20320_at	L20320	fail	1		PASS	9	1	4.89	Normal	Normal	CDK7	2p15-cen	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk- activating kinase)	Kinase
EPHB4	U07695_at	U07695	fail	0		PASS	8	0	6.50	Normal	Normal	EPHB4	7	EphB4	Kinase
PRP4H	U48736_at	U48736	fail	0		PASS	8	0	5.00	Normal	Normal	PRP4		serine/threonine-protein kinase PRP4 homolog	Kinase
BLK	S76617_at	S76617	fail	0		PASS	7	0	4.71	Normal	Normal	BLK	8p23-p22	B lymphoid tyrosine kinase	Kinase
CHED	M80629_at	M80629	fail	3		PASS	10	3	5.30	Normal	Normal	CDC2L		cholinesterase-related cell division controller	Kinase
CLC	L01664_at	L01664	fail	3		PASS	9	3	7.22	Normal	Normal	CLC	19q13.1	Charot-Leyden crystal protein	Kinase
L05624_s	L05624_s_at	L05624	fail	3		PASS	9	3	5.56	Normal	Normal			MAP kinase kinase	Kinase
PLK	U01038_at	U01038	fail	3		PASS	9	3	5.56	Normal	Normal			pLK	Kinase
S80267_s	S80267_s_at	S80267	fail	4		PASS	8	4	4.88	Normal	Normal	p72syk		p72syk	Kinase
CSNK1A1	L37042_at	L37042	fail	4		PASS	7	4	8.00	Normal	Normal	CSNK1A1	13q13	casein kinase 1, alpha 1	Kinase
CSNK2A1	M55265_at	M55265	fail	3		PASS	7	3	5.86	Normal	Normal	CSNK2A1	20p13	casein kinase 2, alpha 1 polypeptide	Kinase
HG4120-HT	HG4120-HT	HG4120-HT	PASS	6	5.17	fail	3	6		Disease	Disease				Kinase
LTK	D16105_at	D16105	PASS	9	23.78	fail	3	9		Disease	Disease	LTK	15	leukocyte tyrosine kinase	Kinase
K60_GNP	D31766_at	D31766	PASS	8	14.50	fail	6	8		Disease	Disease	KIAA0060		KIAA0060 gene product	Kinase
CDK2	M68520_at	M68520	PASS	8	7.63	fail	6	8		Disease	Disease	CDK2	12q13	cyclin-dependent kinase 2	Kinase
PRKACG	M34182_at	M34182	PASS	8	41.00	fail	5	8		Disease	Disease	PRKACG	9q13	protein kinase, cAMP-dependent, catalytic, gamma	Kinase
K213	D86968_at	D86968	PASS	7	4.14	fail	6	7		Disease	Disease	KIAA0213		Similar to Mouse TFIIi-associated transactivator factor p17(GB_RO:MMU11548): Containing protein kinase motif	Kinase
TESK1	D50863_at	D50863	PASS	5	8.80	fail	6	5		Disease	Disease	TESK1	9p13	TESK1, testis-specific kinase 1	Kinase
GCDH	U69141_at	U69141	PASS	5	6.40	fail	4	5		Disease	Disease	GCDH	19p13.2	glutaryl-Coenzym A dehydrogenase	Kinase
ILK	U40282_at	U40282	PASS	9	29.22	PASS	12	9	8.58	3.40	3.40	ILK	11p15.5- p15.4	integrin-linked kinase	Kinase
HCFC1	L20010_at	L20010	PASS	8	26.13	PASS	13	8	8.92	2.93	2.93				Kinase
PRKMK3	D87116_at	D87116	PASS	9	32.89	PASS	11	9	11.27	2.92	2.92	PRKMK3	17q11.2	protein kinase, mitogen-activated, kinase 3 (MAP kinase kinase 3)	Kinase
FAST	X86779_at	X86779	PASS	9	20.33	PASS	10	9	7.30	2.79	2.79	fast		FAST kinase	Kinase
X59932_s	X59932_s_at	X59932	PASS	9	62.44	PASS	13	9	22.46	2.78	2.78	CSK	15q23-q25	c-src tyrosine kinase	Kinase
CSNK2A2	M55268_at	M55268	PASS	9	17.33	PASS	7	9	6.57	2.64	2.64	CSNK2A2	16p13.3- p13.2	casein kinase 2, alpha prime polypeptide	Kinase

K151_SPK	D63485_at	D63485	PASS	9	18.89	PASS	10	9	7.20	2.62	2.62	KIAA0151	6p21	KIAA0151 gene product	Kinase
M16750_s	M16750_s_at	M16750	PASS	9	34.89	PASS	13	9	13.92	2.51	2.51	PIM1	3	pim-1 oncogene	Kinase
RPS6KA2	L07597_at	L07597	PASS	9	28.78	PASS	12	9	11.92	2.41	2.41	RPS6KA1		ribosomal protein S6 kinase, 90kD, polypeptide 1	Kinase
ECGF1_ma	U62317_ma	U62317	PASS	9	66.22	PASS	13	9	27.54	2.40	2.40			arylsulfatase A	Kinase
GLA	X14448_at	X14448	PASS	9	20.56	PASS	13	9	8.62	2.39	2.39			alpha-D-galactosidase A	Kinase
DGK5Z	U51477_at	U51477	PASS	9	32.56	PASS	13	9	13.77	2.36	2.36	DGKZ		diacylglycerol kinase, zeta (104kD)	Kinase
PIM2	U77735_at	U77735	PASS	6	24.33	PASS	12	6	10.33	2.35	2.35			pim-2 protooncogene homolog pim-2h	Kinase
M54915_s	M54915_s_at	M54915	PASS	9	54.67	PASS	13	9	23.54	2.32	2.32			pim-1 protein	Kinase
CAKB	U43522_at	U43522	PASS	8	14.13	PASS	9	8	6.11	2.31	2.31	PTK2B	8p21.1	focal adhesion kinase 2 (protein kinase B)	Kinase
M13829_s	M13829_s_at	M13829	PASS	8	15.25	PASS	13	8	6.69	2.28	2.28	ARAF1	Xp11.4-p11.2	v-rat murine sarcoma 3611 viral oncogene homolog 1	Kinase
AKT1	M63167_at	M63167	PASS	8	23.13	PASS	11	8	10.18	2.27	2.27	AKT1	14q32.3	rac protein kinase-alpha	Kinase
ZAP70	L05148_at	L05148	PASS	9	36.56	PASS	13	9	16.31	2.24	2.24				Kinase
RAD23A	D21235_at	D21235	PASS	9	15.56	PASS	10	9	7.00	2.22	2.22	RAD23A	19p13.2	HHR23A protein,RAD23 (S. cerevisiae) homolog A	Kinase
FGR	M19722_at	M19722	PASS	9	94.78	PASS	13	9	43.00	2.20	2.20	FGR	1p36.2-p36.1	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	Kinase
DAGK1	X62535_at	X62535	PASS	9	38.56	PASS	13	9	17.92	2.15	2.15	DGKA	12	diacylglycerol kinase	Kinase
C8FWPH	AJ000480_at	AJ000480	PASS	5	11.60	PASS	9	5	5.44	2.13	2.13	C8FW		phosphoprotein	Kinase
D63479_s	D63479_s_at	D63479	PASS	9	18.67	PASS	12	9	8.83	2.11	2.11	DGKD		diacylglycerol kinase, delta (130kD)	Kinase
HPK1	U66464_at	U66464	PASS	9	16.89	PASS	13	9	8.00	2.11	2.11	HPK1		hematopoietic progenitor kinase	Kinase
GPRK6	L16862_at	L16862	PASS	7	25.29	PASS	7	7	12.00	2.11	2.11	GPRK6	5q35	G protein-coupled receptor kinase 6	Kinase
IRAK1	L76191_at	L76191	PASS	9	32.67	PASS	13	9	15.54	2.10	2.10	IRAK1	Xq28	interleukin-1 receptor-associated kinase 1	Kinase
P14KB	U81802_at	U81802	PASS	7	14.71	PASS	11	7	7.00	2.10	2.10	PIK4CB	1q21	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	Kinase
Z69043_s	Z69043_s_at	Z69043	PASS	9	57.11	PASS	13	9	27.62	2.07	2.07	H-TRAP delta		translocin-associated protein delta subunit precursor	Kinase
GSK3A	L40027_at	L40027	PASS	9	19.89	PASS	13	9	9.77	2.04	2.04			glycogen synthase kinase 3	Kinase
PIK4	L36151_at	L36151	PASS	9	39.89	PASS	13	9	19.69	2.03	2.03	PIK4CA		phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	Kinase
3PK	U09578_at	U09578	PASS	8	17.25	PASS	13	8	8.54	2.02	2.02	MAPKAPK3	3p21.3	mitogen-activated protein kinase-activated protein kinase 3	Kinase
MLK3	L32976_at	L32976	PASS	7	12.29	PASS	7	7	6.14	2.00	2.00	MLK3	11q13.1-q13.3	mixed lineage kinase 3	Kinase
CLK2	L29218_at	L29218	PASS	7	13.71	PASS	11	7	7.09	1.93	1.93	CLK2	1q21	CDC-like kinase 2	Kinase
K135_PIM	D50925_at	D50925	PASS	6	12.00	PASS	9	6	6.33	1.89	1.89	KIAA0135		The KIAA0135 gene is related to pim-1 oncogene.	Kinase
ZAP112	L40399_at	L40399	PASS	6	26.50	PASS	10	6	14.00	1.89	1.89			ORF, putative	Kinase
CBOGS395	D87119_at	D87119	PASS	8	19.75	PASS	12	8	10.50	1.88	1.88	GS3955		GS3955	Kinase
PRKCD	D10495_at	D10495	PASS	9	30.22	PASS	12	9	16.58	1.82	1.82			protein kinase C delta-type	Kinase
CSNK1D	U29171_at	U29171	PASS	9	18.22	PASS	12	9	10.08	1.81	1.81	CSNK1D	17q25	casein kinase I, delta	Kinase
K96_PK	D43636_at	D43636	PASS	9	15.89	PASS	13	9	9.00	1.77	1.77	KIAA0096		KIAA0096 gene product is related to a protein kinase.	Kinase
FYN	M14676_at	M14676	PASS	9	31.89	PASS	13	9	18.08	1.76	1.76	FYN	6q21	FYN oncogene related to SRC, FGR, YES	Kinase
CSNK1G2	U89896_at	U89896	PASS	6	9.83	PASS	9	6	5.67	1.74	1.74			casein kinase I gamma 2	Kinase

TRNA	STL	U07424_at	U07424	PASS	7	14.00	PASS	11	7	8.09	1.73	1.73	FARSL	phenylalanine-tRNA synthetase-like	Kinase
PKUA		AB004884	AB004884	PASS	7	12.29	PASS	8	7	7.13	1.72	1.72		PKU-alpha	Kinase
U23852_s		U23852_s_at	U23852	PASS	9	66.89	PASS	13	9	38.85	1.72	1.72	lck	p56lck	Kinase
DYRK		D86550_at	D86550	PASS	9	18.67	PASS	13	9	10.85	1.72	1.72	hMNB	serine/threonine protein kinase	Kinase
SLC6A8_m		U36341_m	U36341	PASS	9	13.11	PASS	9	9	7.67	1.71	1.71	SLC6A8	creatine transporter	Kinase
SSBP		M94556_at	M94556	PASS	9	23.78	PASS	13	9	14.15	1.68	1.68	SSBP	single-stranded DNA-binding protein	Kinase
D13720_s		D13720_s_at	D13720	PASS	8	14.25	PASS	13	8	8.62	1.65	1.65		TFK	Kinase
ABR		U01147_at	U01147	PASS	9	9.89	PASS	12	9	6.00	1.65	1.65	ABR	guanine nucleotide regulatory protein	Kinase
M16591_s		M16591_s_at	M16591	PASS	9	29.44	PASS	13	9	17.92	1.64	1.64	HCK	hemopoietic cell kinase	Kinase
X77588_s		X77588_s_at	X77588	PASS	8	10.88	PASS	12	8	6.67	1.63	1.63	ARD1	ARD1 N-acetyl transferase homologue	Kinase
TFE3_m		X97160_m	X97160	PASS	7	9.29	PASS	7	7	6.00	1.55	1.55		TFE3 transcription factor	Kinase
M30448_s		M30448_s_at	M30448	PASS	9	58.11	PASS	13	9	38.38	1.51	1.51	CSNK2B	casein kinase 2, beta polypeptide	Kinase
K137_COS		D50927_at	D50927	PASS	8	10.25	PASS	13	8	6.85	1.50	1.50	KIAA0137	KIAA0137 gene product	Kinase
PAK1		U24152_at	U24152	PASS	9	13.22	PASS	12	9	8.83	1.50	1.50	PAK1	p21/Cdc42/Rac1-activated kinase 1 (yeast Ste20-related)	Kinase
ZPK		U07358_at	U07358	PASS	7	8.86	PASS	11	7	6.09	1.45	1.45	ZPK	serine/threonine protein kinase	Kinase
PSMB10_c		X71874_cds	X71874	PASS	9	73.89	PASS	13	9	51.23	1.44	1.44	PSMB10	proteasome (prosome, macropain) subunit, beta type, 10	Kinase
M36430_s		M36430_s_at	M36430	PASS	7	12.71	PASS	13	7	8.85	1.44	1.44	GNB1	guanine nucleotide binding protein (G protein), beta polypeptide 1	Kinase
RPS6KA2		U08316_at	U08316	PASS	5	8.00	PASS	11	5	5.64	1.42	1.42	RPS6KA3	ribosomal protein S6 kinase, 90kD, polypeptide 3	Kinase
ATP7A		AB000409_at	AB000409	PASS	9	9.89	PASS	10	9	7.10	1.39	1.39	MKNK1	MAP kinase-interacting serine/threonine kinase 1	Kinase
HG3730-HT		HG3730-HT	HG3730-HT	PASS	8	9.75	PASS	12	8	7.08	1.38	1.38			Kinase
LYN		M16038_at	M16038	PASS	9	17.11	PASS	13	9	12.54	1.36	1.36	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	Kinase
D26535_s		D26535_s_at	D26535	PASS	8	10.00	PASS	11	8	7.36	1.36	1.36	DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	Kinase
DYRK2		Y09216_at	Y09216	PASS	6	10.17	PASS	12	6	7.50	1.36	1.36	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	Kinase
BTK_m		U78027_m	U78027	PASS	7	10.71	PASS	12	7	7.92	1.35	1.35	FTP3	FTP3	Kinase
PSKH1		U09564_at	U09564	PASS	8	7.50	PASS	11	8	5.55	1.35	1.35	SRPK1	SFRS protein kinase 1	Kinase
VRK1		AB000449	AB000449	PASS	7	7.57	PASS	10	7	5.90	1.28	1.28	VRK1	vaccinia related kinase 1	Kinase
HNRNPCL		M94630_at	M94630	PASS	9	27.56	PASS	13	9	21.69	1.27	1.27	HNRPD	heterogeneous nuclear ribonucleoprotein D	Kinase
TGFBR2		D50683_at	D50683	PASS	9	24.00	PASS	13	9	18.92	1.27	1.27	TGFBR2	transforming growth factor, beta receptor II (70-80kD)	Kinase
GPRK5		L15388_at	L15388	PASS	6	6.33	PASS	7	6	5.00	1.27	1.27	GPRK5	G protein-coupled receptor kinase	Kinase
HG3484-HT		HG3484-HT	HG3484-HT	PASS	7	8.86	PASS	12	7	7.00	1.27	1.27			Kinase

ATM	U33841_at	U33841	PASS	5	6.20	PASS	9	5	5.11	1.21	1.21	ATM	11q22-q23	ataxia telangiectasia mutated (includes complementation groups A, C and D)	Kinase
DNAPKCS	U47077_at	U47077	PASS	7	5.29	PASS	8	7	4.38	1.21	1.21	PRKDC	8q11	DNA-dependent protein kinase catalytic subunit	Kinase
YES1	M15990_at	M15990	PASS	7	5.43	PASS	7	7	4.71	1.15	1.15	YES1	18p11.31-p11.21	v-src-1 Yamaguchi sarcoma viral oncogene homolog 1	Kinase
PRKMK1	L11284_at	L11284	PASS	7	10.29	PASS	13	7	9.46	1.09	1.09	PRKMK1	15q22.1-q22.33	protein kinase, mitogen-activated, kinase 1 (MAP kinase kinase 1)	Kinase
S203_15	L40395_at	L40395	PASS	8	6.50	PASS	9	8	6.11	1.06	1.06			ORF, putative	Kinase
SRPK2	U88666_at	U88666	PASS	8	5.38	PASS	12	8	5.08	1.06	1.06	SRPK2	7q22-q31.1	SFRS protein kinase 2	Kinase
PAK3	U25975_at	U25975	PASS	5	5.60	PASS	10	5	5.40	1.04	1.04	hPAK65		hPAK65	Kinase
PRKACB	M34181_at	M34181	PASS	5	6.80	PASS	10	5	6.70	1.01	1.01	PRKACB	1	protein kinase, cAMP-dependent, catalytic, beta	Kinase
JAK1	M64174_at	M64174	PASS	5	8.80	PASS	13	5	9.85	0.89	-1.12	JAK1	1p32.3-p31.3	Janus kinase 1 (a protein tyrosine kinase)	Kinase

Phosphatases															
PTPRA	M34668_at	M34668	fail	2		PASS	9	2	5.67	Normal	Normal	PTPRA	20p13	protein tyrosine phosphatase, receptor type, alpha polypeptide	Phosphatase
PTEN	U92436_at	U92436	fail	3		PASS	11	3	5.00	Normal	Normal	PTEN	10q23	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	Phosphatase
PLCD1	U09117_at	U09117	fail	4		PASS	7	4	7.57	Normal	Normal			phospholipase c delta 1	Phosphatase
PTPRE	HG620-HT6	HG620-HT6	fail	3		PASS	7	3	8.00	Normal	Normal				Phosphatase
PLCG2H	U45974_at	U45974	PASS	5	15.40	fail	0	5		Disease	Disease				Phosphatase
PTPRN	L18983_at	L18983	PASS	5	20.00	fail	0	5		Disease	Disease	PTPRN	2q35-q36.1	protein tyrosine phosphatase, receptor type, N	Phosphatase
INPPL1	L36818_at	L36818	PASS	7	21.71	fail	6	7		Disease	Disease			S1C protein	Phosphatase
M33684_s	M33684_s_at	M33684	PASS	5	6.60	fail	3	5		Disease	Disease	PTPNI		non-receptor tyrosine phosphatase 1	Phosphatase
PLCB2	M95678_at	M95678	PASS	9	84.00	PASS	12	9	26.92	3.12	3.12	PLCB2	15q15	phospholipase C, beta 2	Phosphatase
K15_PPM1	D13640_at	D13640	PASS	9	29.00	PASS	12	9	11.33	2.56	2.56	KIAA0015			Phosphatase
PPP4C	X70218_at	X70218	PASS	7	27.43	PASS	11	7	11.18	2.45	2.45	PPP4C	16p12-16p11	protein phosphatase 4 (formerly X), catalytic subunit	Phosphatase
INPP5D	U57650_at	U57650	PASS	9	42.78	PASS	13	9	18.77	2.28	2.28	INPP5D	2q36-q37	SH2-containing inositol 5-phosphatase	Phosphatase
PP1	U14603_at	U14603	PASS	9	76.56	PASS	13	9	35.31	2.17	2.17	PTP4A2	1p35	protein tyrosine phosphatase type IVA, member 2	Phosphatase
J03805_s_at	J03805_s_at	J03805	PASS	9	14.33	PASS	13	9	7.23	1.98	1.98	PPP2CB	8p12-p11.2	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	Phosphatase
M37238_s	M37238_s_at	M37238	PASS	9	11.33	PASS	9	9	6.22	1.82	1.82	PLCG2	16q24.1	phospholipase C, gamma 2 (phosphatidylinositol-specific)	Phosphatase
PTPCAAX	U48296_at	U48296	PASS	7	8.43	PASS	8	7	5.13	1.64	1.64	PTP4A1	6q12	Protein tyrosine phosphatase IVA1	Phosphatase

Table 1. Summary of the results of the analysis of the data from the 1000 Genomes Project.

PPP3CB	S46622_at	S46622	PASS	5	6.40	PASS	10	5	4.40	1.45	1.45	calcineurin A catalytic subunit, calmodulin-dependent protein phosphatase catalytic subunit, CaM-		calcineurin A catalytic subunit	Phosphatase
PTPN12	M93425_at	M93425	PASS	9	16.22	PASS	13	9	11.69	1.39	1.39	PTPN12	7q11.23	protein tyrosine phosphatase, non-receptor type 12	Phosphatase
PPP3CB2	M29551_at	M29551	PASS	5	7.60	PASS	9	5	6.00	1.27	1.27				Phosphatase
PTPN4	M68941_at	M68941	PASS	7	7.86	PASS	9	7	6.56	1.20	1.20	PTPN4		protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	Phosphatase
ACP1	U25849_at	U25849	PASS	6	9.83	PASS	13	6	8.69	1.13	1.13	ACP1	2p25	acid phosphatase 1, soluble	Phosphatase
M60483_m	M60483_ma	M60483	PASS	8	6.50	PASS	12	8	5.75	1.13	1.13	PPP2CA	5q23-q31	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	Phosphatase
D11327_s	D11327_s_a	D11327	PASS	8	5.75	PASS	10	8	5.10	1.13	1.13	PTPN7	1q32.1	protein tyrosine phosphatase, non-receptor type 7	Phosphatase
PPM1A	S87759_at	S87759	PASS	7	6.00	PASS	9	7	5.33	1.13	1.13	PPM1B		protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	Phosphatase

Table 3

HuPBMc RA U95A-Kin-PhosP.xls

Human RA PBMC data on U95										Human RA PBMC data on U95									
Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (Normal)	Fold Change RA / Normal	Name	Chromosome	Kinase or Phosphatase			
Kinases	446_at	CSNK1G2	6	Pass	9.17	3.54	13	Pass	TRUE	FALSE	FALSE	4.69	1.95	casein kinase 1, gamma 2; CSNK1G2	19p13.3	Kinase			
	490_g_at	MUTYH	6	Pass	11.00	2.97	13	Pass	TRUE	FALSE	FALSE	5.62	1.96	mutY (E. coli) homolog; MUTYH	1p34.3-p32.1	Kinase			
	41197_at	RAD23A	6	Pass	18.50	4.32	13	Pass	TRUE	FALSE	FALSE	9.38	1.97	RAD23 (S. cerevisiae) homolog A; RAD23A	19p13.2	Kinase			
	33300_at	CDC2L1	6	Pass	11.83	3.76	12	Pass	TRUE	FALSE	FALSE	5.92	2.00	Cluster Incl AL031282: Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, and GSSs, complete sequence.		Kinase			
	40742_at	HCK	6	Pass	52.50	31.65	13	Pass	TRUE	FALSE	FALSE	25.92	2.03	hemopoietic cell kinase; HCK	20q11-q12	Kinase			
32799_at	C1ORF2	6	Pass	24.17	6.43	11	Pass	TRUE	TRUE	FALSE	FALSE	11.91	2.03	secretory carrier membrane protein 3; kinase kinase 3; MAP2K3		Kinase			
1622_at	MAP2K3	6	Pass	40.17	14.39	13	Pass	TRUE	TRUE	FALSE	FALSE	19.77	2.03	mitogen-activated protein kinase kinase 3; MAP2K3	17q11.2	Kinase			
146_at	PIK4CB	6	Pass	6.33	1.75	9	Pass	TRUE	TRUE	FALSE	FALSE	3.11	2.04	phosphatidylinositol 4-kinase, catalytic, beta polypeptide; PIK4CB	1q21	Kinase			
1392_at	GPRK6	4	Pass	28.25	5.50	7	Pass	TRUE	TRUE	FALSE	FALSE	13.86	2.04	G protein-coupled receptor kinase 6; GPRK6	5q35	Kinase			
33314_at	GCDH	6	Pass	6.17	1.17	11	Pass	TRUE	TRUE	FALSE	FALSE	3.00	2.06	glutaryl-Coenzyme A dehydrogenase; GCDH	19p13.2	Kinase			
34808_at	KIAA0999	6	Pass	12.50	2.51	13	Pass	TRUE	TRUE	FALSE	FALSE	6.08	2.06	KIAA0999 protein; KIAA0999		Kinase			
32046_at	PRKCD	6	Pass	26.83	9.93	13	Pass	TRUE	TRUE	FALSE	FALSE	13.00	2.06	protein kinase C, delta; PRKCD	3p	Kinase			
384_at	PSMB10	6	Pass	50.00	22.63	13	Pass	TRUE	TRUE	FALSE	FALSE	24.15	2.07	proteasome (prosome, macropain) subunit, beta type, 10; PSMB10	16q22.1	Kinase			
41249_at	UNK AL0	6	Pass	25.67	13.23	13	Pass	TRUE	TRUE	FALSE	FALSE	12.31	2.09			Kinase			
32716_at	DGKA	6	Pass	46.33	9.56	13	Pass	TRUE	TRUE	FALSE	FALSE	22.08	2.10	diacylglycerol kinase, alpha (80kD); DGKA	12q13.3	Kinase			
1779_s_at	PIM1	6	Pass	42.00	9.61	13	Pass	TRUE	TRUE	FALSE	FALSE	20.00	2.10	pim-1 oncogene; PIM1	6p21.2	Kinase			
31873_at	ARD1	6	Pass	8.67	2.50	11	Pass	TRUE	TRUE	FALSE	FALSE	4.09	2.12			Kinase			
187_at	MAP4K2	5	Pass	5.80	1.30	7	Pass	TRUE	TRUE	FALSE	FALSE	2.71	2.14	mitogen-activated protein kinase kinase kinase	11q13	Kinase			
37910_at	HCFC1	6	Pass	8.17	3.60	11	Pass	TRUE	TRUE	FALSE	FALSE	3.82	2.14	kinase 2; MAP4K2		Kinase			
1780_at	FGR	6	Pass	80.83	35.22	13	Pass	TRUE	TRUE	FALSE	FALSE	37.77	2.14	host cell factor C1 (VPI6-accessory protein); Gardner-Rasheed feline sarcoma viral (v-lgr) oncogene homolog; FGR	Xq28	Kinase			
33281_at	KIAA0151	6	Pass	14.33	1.63	13	Pass	TRUE	TRUE	FALSE	FALSE	6.69	2.14	IKK-related kinase epsilon; inducible IkkappaB kinase; IKKE	1	Kinase			
39044_s_at	DGKD	6	Pass	31.67	7.76	13	Pass	TRUE	TRUE	FALSE	FALSE	14.77	2.14	diacylglycerol kinase, delta (130kD); DGKD		Kinase			
40420_at	STK10	6	Pass	35.17	8.70	13	Pass	TRUE	TRUE	FALSE	FALSE	16.38	2.15	serine/threonine kinase 10; STK10	5q35.1	Kinase			
40225_at	GAK	6	Pass	37.17	12.67	13	Pass	TRUE	TRUE	FALSE	FALSE	17.31	2.15	cyclin G associated kinase; GAK	4p16	Kinase			
632_at	GSK3A	6	Pass	19.00	5.69	13	Pass	TRUE	TRUE	FALSE	FALSE	8.77	2.17	glycogen synthase kinase 3 alpha; GSK3A		Kinase			

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35796_at	PTK9L	Y17169	6	Pass	16.17	9.54	12	Pass	TRUE	FALSE	FALSE	7.42	protein tyrosine kinase 9-like (A6-related protein); PTK9L	3p21.1	Kinase *
2075_s_at	MAP2K3	L36719	6	Pass	17.67	4.23	12	Pass	TRUE	FALSE	FALSE	8.00	mitogen-activated protein kinase kinase 3; MAP2K3	17q11.2	Kinase *
33301_s_at	CDC2L1	AL031282	6	Pass	21.50	7.34	13	Pass	TRUE	FALSE	FALSE	9.69	Cluster Incl AL031282: Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIER1-2		Kinase
1810_s_at	PRKCD	D10495	6	Pass	14.00	5.62	11	Pass	TRUE	FALSE	FALSE	6.27	protein kinase C, delta; PRKCD	3p	Kinase
36949_at	CSNK1D	U29171	6	Pass	45.00	11.93	13	Pass	TRUE	FALSE	FALSE	20.08	casein kinase 1, delta; CSNK1D	17q25	Kinase
1707_s_at	ARAF1	U01337	6	Pass	31.00	6.75	11	Pass	TRUE	FALSE	FALSE	13.82	v-rat murine sarcoma 3611 viral oncogene homolog 1; ARAF1 Ser/Thr protein kinase	Xp11.4-p11.2	Kinase
38617_at	LIMK2	D45906	5	Pass	9.00	2.55	11	Pass	TRUE	FALSE	FALSE	4.00	LIM domain kinase 2; LIMK2	22q12.2	Kinase
35299_at	MKNK1	AB000409	6	Pass	8.67	2.73	12	Pass	TRUE	FALSE	FALSE	3.83	MAP kinase-interacting serine/threonine kinase 1; MKNK1		Kinase *
34291_at	FARSL	U07424	6	Pass	11.00	3.35	13	Pass	TRUE	FALSE	FALSE	4.77	phenylalanine-tRNA synthetase-like; FARSL	19p13.2	Kinase
1498_at	ZAP70	L05148	6	Pass	35.67	9.71	13	Pass	TRUE	FALSE	FALSE	15.38	zeta-chain (TCR) associated protein kinase (70 kD); ZAP70	2q12	Kinase *
1706_at	ARAF1	U01337	6	Pass	25.17	6.43	13	Pass	TRUE	FALSE	FALSE	10.69	v-rat murine sarcoma 3611 viral oncogene homolog 1; ARAF1	Xp11.4-p11.2	Kinase
1127_at	RPS6KA1	L07597	6	Pass	33.67	13.82	13	Pass	TRUE	FALSE	FALSE	14.15	ribosomal protein S6 kinase, 90kD, polypeptide 1; RPS6KA1	3	Kinase
36179_at	MAPKAPK2	U12779	6	Pass	36.67	8.19	13	Pass	TRUE	FALSE	FALSE	15.31	mitogen-activated protein kinase-activated protein kinase 2; MAPKAPK2		Kinase *
1652_at	PIM2	U77735	6	Pass	17.50	7.82	11	Pass	TRUE	FALSE	FALSE	7.27	pim-2 oncogene; PIM2	X	Kinase
883_s_at	PIM1	M54915	6	Pass	59.00	8.44	13	Pass	TRUE	FALSE	FALSE	24.46	pim-1 oncogene; PIM1	6p21.2	Kinase
33804_at	PTK2B	U43522	6	Pass	16.67	7.63	8	Pass	TRUE	FALSE	FALSE	6.88	protein tyrosine kinase 2 beta; PTK2B	8p21.1	Kinase *
493_at	CSNK1D	U29171	6	Pass	17.17	6.43	13	Pass	TRUE	FALSE	FALSE	7.08	casein kinase 1, delta; CSNK1D	17q25	Kinase
1398_s_at	MAP3K11	L32976	6	Pass	27.83	17.62	13	Pass	TRUE	FALSE	FALSE	11.46	mitogen-activated protein kinase kinase kinase 11; MAP3K11	11q13.1-q13.3	Kinase
33903_at	DAPK3	AB007144	5	Pass	13.00	5.61	9	Pass	TRUE	FALSE	FALSE	5.22	death-associated protein kinase 3; DAPK3	19p13.3	Kinase *
1134_at	ACK1	L13738	6	Pass	25.00	7.07	12	Pass	TRUE	FALSE	FALSE	10.00	activated p21cdc42Hs kinase; ACK1	3	Kinase
33223_at	KIAA0561	AB011133	6	Pass	16.17	7.17	13	Pass	TRUE	FALSE	FALSE	6.46	KIAA0561 protein;		Kinase
32004_s_at	UNK_W32	W32483	6	Pass	10.83	5.04	13	Pass	TRUE	FALSE	FALSE	4.31			Kinase
34679_at	BCR	X02596	5	Pass	17.00	2.00	12	Pass	TRUE	FALSE	FALSE	6.67	breakpoint cluster region; BCR	22q11.23	Kinase
35365_at	ILK	U40282	6	Pass	30.17	5.98	13	Pass	TRUE	FALSE	FALSE	11.62	integrin-linked kinase; ILK	11p15.5-p15.4	Kinase *

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38269_at	DKFZP586AL050147	AL050147	6	Pass	44.67	9.63	13	TRUE	FALSE	16.92	2.64	DKFZP586E0820 protein; 19	19	Kinase
1768_s_at	CSK	X59932	6	Pass	75.50	29.19	13	TRUE	FALSE	27.77	2.72	c-src tyrosine kinase; CSK	15q23-q25	Kinase
38003_s_at	DGKZ	U94905	6	Pass	29.17	12.50	13	TRUE	FALSE	10.23	2.85	diacylglycerol kinase, zeta (104kD); DGKZ		Kinase
138_at	MAP4K1	U66464	6	Pass	16.33	4.13	13	TRUE	FALSE	5.69	2.87	mitogen-activated protein kinase kinase kinase 1; MAP4K1	19q13.1-q13.4	Kinase
993_at	TYK2	X54637	6	Pass	15.50	5.24	12	TRUE	FALSE	5.25	2.95	tyrosine kinase 2; TYK2	19p13.2	Kinase
40235_at	ACK	L13738	6	Pass	13.33	5.05	10	TRUE	FALSE	3.70	3.60	activated p21cdc42Hs kinase; ACK1	3	Kinase

Phosphatases

37384_at	KIAA0015	D13640	6	Pass	18.00	5.40	10	TRUE	FALSE	8.80	2.05	KIAA0015 gene product; KIAA0015	22q11.22	Phosphatase
172_at	INPP5D	U57650	6	Pass	33.00	10.08	13	TRUE	FALSE	16.08	2.05	inositol polyphosphate-5-phosphatase, 145kD; INPP5D	2q36-q37	Phosphatase
41162_at	PPM1G	Y13936	6	Pass	20.00	4.05	13	TRUE	FALSE	9.23	2.17	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; PPM1G		Phosphatase
382_at	PPP4C	X70218	6	Pass	16.83	7.36	13	TRUE	FALSE	7.46	2.26	protein phosphatase 4 (formerly X), catalytic subunit; PPP4C	16p12-16p11	Phosphatase
210_at	PLCB2	M95678	6	Pass	49.17	20.53	12	TRUE	FALSE	20.58	2.39	phospholipase C, beta 2; PLCB2	15q15	Phosphatase
41225_at	UNK_AL0	AL049417	6	Pass	9.17	4.88	13	TRUE	FALSE	3.77	2.43	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related); DUSP3	17q21	Phosphatase
794_at	PTPN6	X62055	6	Pass	28.50	11.93	13	TRUE	FALSE	10.69	2.67	protein tyrosine phosphatase, non-receptor type 6; PTPN6	12p13	Phosphatase
1005_at	DUSP1	X68277	6	Pass	21.17	21.76	13	TRUE	FALSE	6.46	3.28	dual specificity phosphatase 1; DUSP1	5q34	Phosphatase

37864_s_at	IGHG3	Y14737	6	Pass	93.83	76.26	13	TRUE	FALSE	8.00	11.73	immunoglobulin heavy constant gamma 3 (G3m marker); IGHG3	14q32.33	
36482_s_at	ATP2A3	Y15724	6	Pass	17.00	5.33	12	TRUE	FALSE	3.25	5.23	ATPase, Ca++ transporting, ubiquitous; ATP2A3	17p13.3	
40644_g_at	ITGA2B	M34480	6	Pass	37.83	9.95	11	TRUE	FALSE	7.45	5.08	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41B); ITGA2B	17q21.32	
32749_s_at	FLNA	AL050396	6	Pass	209.83	58.51	13	TRUE	FALSE	41.46	5.06	Filamin A, alpha (actin-binding protein-280); FLNA	Xq28	
33501_r_at	IGHA1	S71043	6	Pass	138.50	88.39	13	TRUE	FALSE	28.92	4.79	immunoglobulin heavy constant alpha 1; IGH A1	14q32.33	
33822_at	NUMA1	Z11584	6	Pass	11.50	6.35	12	TRUE	FALSE	2.42	4.76	nuclear mitotic apparatus protein 1; NUMA1	11q13	
38487_at	KIAA0246	D87433	6	Pass	35.50	24.04	8	TRUE	FALSE	7.63	4.66	Stabilin-1		
1268_at	UBE1	M58028	6	Pass	47.50	14.10	13	TRUE	FALSE	10.54	4.51	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity	Xp11.23	
37467_at	IGHD	K02882	6	Pass	25.17	37.82	10	TRUE	FALSE	5.60	4.49	immunoglobulin heavy constant delta; IGH D	14q32.33	

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32378_at	PKM2	M26252	6	Pass	96.17	29.53	13	Pass	TRUE	FALSE	21.77	4.42	pyruvate kinase, muscle; PKM2	15q22	
39049_at	NOTCH4	AJ243937	6	Pass	47.33	13.25	13	Pass	TRUE	FALSE	11.31	4.19	Notch (Drosophila) homolog 4; NOTCH4	6p21.3	
33499_s_at	IGHA1	AF067420	6	Pass	123.33	74.06	13	Pass	TRUE	FALSE	29.62	4.16	immunoglobulin heavy constant alpha 1; IGH A1	14q32.33	
36028_at	TCIRG1	U45285	6	Pass	33.17	17.12	13	Pass	TRUE	FALSE	8.00	4.15	T-cell, immune regulator 1; TCIRG1	11q13.4-q13.5	
32070_at	PTPRCAP	X97267	6	Pass	119.83	16.22	13	Pass	TRUE	FALSE	28.92	4.14	protein tyrosine phosphatase, receptor type, c polypeptide-associated protein; PTPRCAP	11q13.3	
32588_s_at	BRF2	X78992	6	Pass	105.50	33.35	13	Pass	TRUE	FALSE	25.62	4.12	butyrate response factor 2 (EGF-response factor 2); BRF2		
37014_at	MX1	M33882	6	Pass	27.50	22.98	13	Pass	TRUE	FALSE	6.69	4.11	myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible protein p78);	21q22.3	
32623_at	GABBR1	AJ225028	6	Pass	18.17	4.17	7	Pass	TRUE	FALSE	4.43	4.10	gamma-aminobutyric acid (GABA) B receptor, 1; GABBR1	6p21.3	
596_s_at	CSF3R	M59820	6	Pass	40.67	20.97	12	Pass	TRUE	FALSE	9.92	4.10	colony stimulating factor 3 receptor (granulocyte); CSF3R	1p35-p34.3	
1915_s_at	FOS	V01512	6	Pass	63.50	46.86	13	Pass	TRUE	FALSE	15.54	4.09	v-fos FBJ murine osteosarcoma viral oncogene homolog; FOS	14q24.3	
36412_s_at	IRF7	U53831	6	Pass	17.00	10.66	12	Pass	TRUE	FALSE	4.17	4.08	interferon regulatory factor 7; IRF7	11	
36138_at	CAPN4	X04106	6	Pass	57.67	25.33	13	Pass	TRUE	FALSE	14.38	4.01	calpain, small polypeptide; CAPN4	19	
36879_at	ECGF1	M63193	6	Pass	89.00	78.82	12	Pass	TRUE	FALSE	22.33	3.99	endothelial cell growth factor 1 (platelet-derived); ECGF1	22q13.33	
1916_s_at	FOS	V01512	6	Pass	46.17	29.96	13	Pass	TRUE	FALSE	12.00	3.85	v-fos FBJ murine osteosarcoma viral oncogene homolog; FOS	14q24.3	
33273_f_at	IGL@	X57809	6	Pass	180.83	155.56	13	Pass	TRUE	FALSE	47.38	3.82	immunoglobulin lambda locus; IGL@	22q11.1-q11.2	
34874_at	NTE	AJ004832	6	Pass	23.00	12.44	12	Pass	TRUE	FALSE	6.08	3.78	neuropathy target esterase; NTE	19p	
41827_f_at	UNK A193	AJ932613	6	Pass	58.67	49.98	13	Pass	TRUE	FALSE	15.69	3.74	SMA3; SMA3	5q13	
38647_at	COPE	AJ131182	6	Pass	44.83	17.38	13	Pass	TRUE	FALSE	12.00	3.74	coatamer protein complex, subunit epsilon; COPE		
40164_at	ARHGDIA	X09550	6	Pass	42.17	14.66	13	Pass	TRUE	FALSE	11.31	3.73	Rho GDP dissociation inhibitor (GDI) alpha; ARHGDIA	17q25.3	
33500_i_at	IGHA1	S71043	6	Pass	109.33	64.26	13	Pass	TRUE	FALSE	30.00	3.64	immunoglobulin heavy constant alpha 1; IGH A1	14q32.33	
40718_at	CTSW	AF013611	6	Pass	30.50	19.00	10	Pass	TRUE	FALSE	8.40	3.63	cathepsin W (kynphosin); CTSW	11q13.1	
33143_s_at	SLC16A3	U81800	6	Pass	43.83	23.80	13	Pass	TRUE	FALSE	12.15	3.61	solute carrier family 16 (monocarboxylic acid transporters), member 3; SLC16A3	22q12.3-q13.2	
239_at	CTSD	M63138	6	Pass	76.50	38.12	13	Pass	TRUE	FALSE	21.31	3.59	cathepsin D (lysosomal aspartyl protease); CTSD	11p15.5	
33816_at	UNK AF0	AF020267	6	Pass	17.33	8.45	12	Pass	TRUE	FALSE	4.92	3.53	myosin IXB; MYO9B	19p13.1	
33283_at	ARRB2	AF106941	6	Pass	84.00	41.95	13	Pass	TRUE	FALSE	24.00	3.50	arrestin, beta 2; ARRB2	17p13	
32750_r_at	FLNA	X53416	6	Pass	23.00	3.95	10	Pass	TRUE	FALSE	6.60	3.48	filamin A, alpha (actin-binding protein-280); FLNA	Xq28	

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31874_at	GAR22	Y07846	6	Pass	15.67	5.82	12	Pass	TRUE	FALSE	FALSE	4.50	3.48	GAS2-related on chromosome 22; GAR22	22q12.2	
39997_at	PFC	AF005664	6	Pass	57.00	28.64	13	Pass	TRUE	FALSE	FALSE	16.69	3.41	properdin P factor; complement; PFC	Xp11.3-p11.23	
41045_at	SECTM1	U77643	6	Pass	29.67	22.56	13	Pass	TRUE	FALSE	FALSE	8.69	3.41	secreted and transmembrane 1;	17q25	
34412_s_at	GP1BB	U59632	6	Pass	85.50	35.30	13	Pass	TRUE	FALSE	FALSE	25.08	3.41	glycoprotein Ib (platelet); beta polypeptide; GP1BB	22q11.21	
33274_f_at	IGL@	M18645	6	Pass	162.50	133.56	13	Pass	TRUE	FALSE	FALSE	48.15	3.37	immunoglobulin lambda locus; IGL@	22q11.1-q11.2	
35170_at	MAN2C1	AF044414	6	Pass	21.50	5.43	10	Pass	TRUE	FALSE	FALSE	6.40	3.36	mannosidase, alpha. class 2C, member 1; MAN2C1	15q11-q13	
41168_at	TAPBP	AF029750	6	Pass	112.50	29.72	13	Pass	TRUE	FALSE	FALSE	34.00	3.31	TAP binding protein (tapasin); TAPBP	6p21.3	
37192_at	EPB49	U28389	6	Pass	56.67	18.65	12	Pass	TRUE	FALSE	FALSE	17.17	3.30	erythrocyte membrane protein band 4.9 (dema1n); EPB49	8p21.1	
38138_at	S100A11	D38583	6	Pass	74.83	42.88	13	Pass	TRUE	FALSE	FALSE	22.77	3.29	S100 calcium-binding protein A11 (calgizzarin); S100A11	1q21	
41446_f_at	RNAHP	H68340	6	Pass	25.67	13.92	13	Pass	TRUE	FALSE	FALSE	7.85	3.27	RNA helicase-related protein; RNAHP	17	
40643_at	ITGA2B	M34480	6	Pass	101.33	18.45	13	Pass	TRUE	FALSE	FALSE	31.00	3.27	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41B); ITGA2B	17q21.32	
37966_at	UNK_AA1	AA187563	6	Pass	10.17	3.43	8	Pass	TRUE	FALSE	FALSE	3.13	3.25	CGI-56 protein; CGI-56	22q13.2-q13.33	
33425_at	T1F1B	X97548	6	Pass	30.67	7.53	13	Pass	TRUE	FALSE	FALSE	9.46	3.24	KRAB-associated protein 1; T1F1B	5	
36493_at	LSP1	M33552	6	Pass	49.17	23.56	13	Pass	TRUE	FALSE	FALSE	15.31	3.21	lymphocyte-specific protein 1; LSP1	11p15.5	
34223_at	CSF3R	M59818	6	Pass	34.33	16.75	13	Pass	TRUE	FALSE	FALSE	10.69	3.21	colony stimulating factor 3 receptor (granulocyte); CSF3R	1p35-p34.3	
34780_at	PLXNB2	AB002313	6	Pass	43.67	21.77	13	Pass	TRUE	FALSE	FALSE	13.62	3.21	plexin B2; PLXNB2	22q13.33	
39649_at	ARHGAP4	X78817	6	Pass	53.00	19.42	13	Pass	TRUE	FALSE	FALSE	16.54	3.20	Rho GTPase activating protein 4; ARHGAP4	Xq28	
35786_at	KIAA0476	AB007945	6	Pass	28.33	9.29	13	Pass	TRUE	FALSE	FALSE	8.85	3.20	KIAA0476 gene product; KIAA0476	1	
39424_at	TNFRSF14	U70321	6	Pass	26.50	9.81	13	Pass	TRUE	FALSE	FALSE	8.31	3.19	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator); TNFRSF14	1p36.3-p36.2	
1353_g_at	IL8RA	U11870	4	Pass	12.75	2.22	8	Pass	TRUE	FALSE	FALSE	4.00	3.19	interleukin 8 receptor, alpha; IL8RA	2q35	
35292_at	D6S81E	Z37166	6	Pass	29.83	5.04	13	Pass	TRUE	FALSE	FALSE	9.38	3.18	HLA-B associated transcript-1; D6S81E	6p21.3	
33438_at	WBP2	AL049981	6	Pass	59.50	19.79	13	Pass	TRUE	FALSE	FALSE	18.77	3.17	WW domain binding protein 2; WBP2	17q25	
36372_at	HK3	U51333	6	Pass	53.83	35.92	12	Pass	TRUE	FALSE	FALSE	17.00	3.17	hexokinase 3 (white cell); HK3	5q35.2	
39182_at	EMP3	U87947	6	Pass	155.83	50.34	13	Pass	TRUE	FALSE	FALSE	49.23	3.17	epithelial membrane protein 3; EMP3	19q13.3	
36229_at	IL17R	U58917	4	Pass	12.25	8.10	8	Pass	TRUE	FALSE	FALSE	3.88	3.16	interleukin 17 receptor; IL17R	22q11.1	
33371_s_at	RAB31	U59877	6	Pass	34.17	14.36	13	Pass	TRUE	FALSE	FALSE	10.85	3.15	RAB31, member RAS oncogene family; RAB31	18p11.3	
40332_at	7-60	AF109134	6	Pass	35.33	18.54	9	Pass	TRUE	FALSE	FALSE	11.22	3.15	7-60 protein; 22098	20q13.3	
810_at	ARHGEF1	U64105	6	Pass	27.83	5.49	13	Pass	TRUE	FALSE	FALSE	8.85	3.15	Rho guanine nucleotide exchange factor (GEF) 1; ARHGEF1	19q13.13	

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36960_at	EDR2	U89278	6	Pass	13.17	7.83	13	TRUE	FALSE	FALSE	4.23	3.11	early development regulator 2 (homolog of polyhormone 2); EDR2	1	
36785_at	HSPB1	Z23090	6	Pass	22.67	9.07	13	TRUE	FALSE	FALSE	7.31	3.10	heat shock 27kD protein 1; 7q	7q	
39082_at	ANXA6	Y00097	6	Pass	62.00	12.18	13	TRUE	FALSE	FALSE	20.15	3.08	HSPB1		
39400_at	KIAA1055	AB028978	6	Pass	11.33	4.27	13	TRUE	FALSE	FALSE	3.69	3.07	annexin A6; ANXA6	5q32-q34	
41106_at	KCNK4	AF022797	5	Pass	10.20	5.36	9	TRUE	FALSE	FALSE	3.33	3.06	KIAA1055 protein; KIAA1055	15	
39076_s_at	DRAP1	A1991040	6	Pass	25.17	8.33	13	TRUE	FALSE	FALSE	8.23	3.06	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4; KCNN4	19q13.2	
39112_at	USF2	Y07661	6	Pass	15.00	4.43	13	TRUE	FALSE	FALSE	4.92	3.05	DRI-associated protein 1 (negative cofactor 2 alpha); DRAP1	11	
38813_at	TSC2	X75621	6	Pass	9.67	2.16	10	TRUE	FALSE	FALSE	3.20	3.02	upstream transcription factor 2, c-fos interacting; USF2	19q13	
34789_at	PI6	S69272	6	Pass	23.83	10.76	13	TRUE	FALSE	FALSE	7.92	3.01	tuberosclerosis 2; TSC2	16p13.3	
37145_at	GNLY	M85276	6	Pass	111.17	70.80	13	TRUE	FALSE	FALSE	37.00	3.00	protease inhibitor 6 (placental thrombin inhibitor); PI6	6p25	
34707_at	CHD3	U91543	6	Pass	21.83	7.25	13	TRUE	FALSE	FALSE	7.31	2.99	granulysin; GNLY	2p12-q11	
38069_at	CLCN7	Z67743	6	Pass	29.83	6.77	11	TRUE	FALSE	FALSE	10.00	2.98	chromodomain helicase DNA binding protein 3; CHD3	17p13.1	
38063_at	UNK_U00	U00952	6	Pass	28.17	12.42	13	TRUE	FALSE	FALSE	9.46	2.98		16p13	
37281_at	KIAA0233	D87071	6	Pass	36.33	11.18	13	TRUE	FALSE	FALSE	12.23	2.97	KIAA0233 gene product; KIAA0233	16	
38194_s_at	IGKV1D-8	M63438	6	Pass	142.17	69.87	13	TRUE	FALSE	FALSE	47.92	2.97	immunoglobulin kappa variable ID-8; IGKV1D-8	2p12	
37411_at	KIAA0050	D30758	6	Pass	34.33	9.40	12	TRUE	FALSE	FALSE	11.58	2.96	KIAA0050 gene product; KIAA0050		
36473_at	USP20	AB023220	6	Pass	16.17	3.66	12	TRUE	FALSE	FALSE	5.50	2.94	ubiquitin specific protease 20; USP20		
36152_at	GD11	X79353	6	Pass	47.83	11.89	13	TRUE	FALSE	FALSE	16.31	2.93	GDP dissociation inhibitor 1; GDI1	Xq28	
35530_f_at	IGL@	X92997	6	Pass	30.17	22.56	11	TRUE	FALSE	FALSE	10.36	2.91	immunoglobulin lambda locus; IGL@	22q11.1-q11.2	
40791_at	POLR2A	X63564	6	Pass	23.50	10.37	13	TRUE	FALSE	FALSE	8.08	2.91	polymerase (RNA) II (DNA directed) polypeptide A (220kD); POLR2A	17p13.1	
41753_at	ACTN4	U48734	6	Pass	30.83	12.92	13	TRUE	FALSE	FALSE	10.69	2.88	actinin, alpha 4; ACTN4	19q13	
33925_at	NRGN	X99076	6	Pass	220.17	53.81	13	TRUE	FALSE	FALSE	76.77	2.87	neurogranin (protein kinase C substrate, RC3);	11q24	
39689_at	CST3	A1362017	6	Pass	65.50	33.53	13	TRUE	FALSE	FALSE	22.85	2.87	cystatin C (amyloid angiopathy and cerebral hemorrhage); CST3	20p11.2	
1107_s_at	ISG15	M13755	6	Pass	39.67	28.62	13	TRUE	FALSE	FALSE	13.85	2.86	interferon-stimulated protein, 15 kDa; ISG15	1	
336_at	TBXA2R	D38081	5	Pass	11.80	2.59	7	TRUE	FALSE	FALSE	4.14	2.85	thromboxane A2 receptor; TBXA2R	19p13.3	
31315_at	UNK_D84	D84143	5	Pass	22.00	16.09	8	TRUE	FALSE	FALSE	7.75	2.84	H1 histone family, member X; H1FX		
319_g_at	H1FX	D64142	6	Pass	86.17	25.13	13	TRUE	FALSE	FALSE	30.46	2.83			
36781_at	PI	X01683	6	Pass	101.67	57.50	13	TRUE	FALSE	FALSE	36.00	2.82	protease inhibitor 1 (anti-elastase), alpha-1-antitrypsin; PI	14q32.1	

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41138_at	MIC2	M16279	6	Pass	74.50	25.15	13	Pass	TRUE	FALSE	FALSE	26.38	2.82	antigen identified by monoclonal antibodies Yp11.3	Xp22.32, Yp11.3	
41198_at	GRN	AF055008	6	Pass	69.00	41.70	11	Pass	TRUE	FALSE	FALSE	24.45	2.82	12E7, F21 and O13; MIC2 granulin; GRN	17	
1294_at	UBE1L	L13852	6	Pass	22.83	3.92	10	Pass	TRUE	FALSE	FALSE	8.10	2.82	ubiquitin-activating enzyme E1, like; UBE1L	3p21	
38894_g_at	NCF4	AL008637	6	Pass	18.83	7.91	13	Pass	TRUE	FALSE	FALSE	6.69	2.81	neutrophil cytosolic factor 4 (40kD); NCF4	22q13.1	
40668_s_at	CD6	U34624	4	Pass	11.00	4.76	11	Pass	TRUE	FALSE	FALSE	3.91	2.81	CD6 antigen; CD6	11q13	
38671_at	KIAA0620	AB014520	6	Pass	11.00	10.24	11	Pass	TRUE	FALSE	FALSE	3.91	2.81	KIAA0620 protein;		
38686_at	ATP6DV	X71490	6	Pass	31.17	16.81	11	Pass	TRUE	FALSE	FALSE	11.09	2.81	Vacuolar proton-ATPase, subunit D; V-ATPase, subunit D; ATP6DV		
35132_at	MYOIE	X98411	6	Pass	94.33	40.45	13	Pass	TRUE	FALSE	FALSE	33.62	2.81	myosin IE; MYOIE		
34405_at	USP5	U47927	6	Pass	14.00	2.68	10	Pass	TRUE	FALSE	FALSE	5.00	2.80	ubiquitin specific protease 5 (isopeptidase T); USP5	12p13	
40667_at	CD6	X60992	6	Pass	31.83	11.62	13	Pass	TRUE	FALSE	FALSE	11.38	2.80	CD6 antigen; CD6	11q13	
31610_at	DD96	U21049	6	Pass	21.67	9.00	12	Pass	TRUE	FALSE	FALSE	7.75	2.80	epithelial protein up-regulated in carcinoma, membrane associated protein 17; DD96	1	
39127_f_at	PPP2R4	X73478	6	Pass	25.33	13.09	13	Pass	TRUE	FALSE	FALSE	9.08	2.79	protein phosphatase 2A, regulatory subunit B' (PR 53); PPP2R4	9q34	
36902_at	ARHG	X61587	6	Pass	42.67	17.57	13	Pass	TRUE	FALSE	FALSE	15.31	2.79	ras homolog gene family, member G (rho G); ARHG	11p15.5-pl5.4	
37387_g_at	KDELR1	X55885	6	Pass	14.17	5.56	12	Pass	TRUE	FALSE	FALSE	5.08	2.79	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1; KDELR1	19q13.3	
33535_at	P2RX1	U45448	6	Pass	9.17	4.17	10	Pass	TRUE	FALSE	FALSE	3.30	2.78	purinergic receptor P2X, ligand-gated ion channel, 1; P2RX1	17p	
36940_at	TIAF1	D86970	6	Pass	5.83	1.83	10	Pass	TRUE	FALSE	FALSE	2.10	2.78	TGFB1-induced anti-apoptotic factor 1; TIAF1	17	
39770_at	KIAA0250	D87437	6	Pass	8.83	3.97	11	Pass	TRUE	FALSE	FALSE	3.18	2.78	KIAA0250 gene product; KIAA0250		
39119_s_at	NK4	AA631972	6	Pass	79.33	22.00	13	Pass	TRUE	FALSE	FALSE	28.62	2.77	natural killer cell transcript 4; NK4	16p13.3	
41850_s_at	DIPA	U63825	6	Pass	12.33	5.39	11	Pass	TRUE	FALSE	FALSE	4.45	2.77	hepatitis delta antigen-interacting protein A;	11	
36843_at	SIPA1	AB005666	6	Pass	12.83	5.67	11	Pass	TRUE	FALSE	FALSE	4.64	2.77	signal-induced proliferation-associated interferon-induced protein with tetratricopeptide repeats 4; IFIT4	11q13.3	
38584_at	IFIT4	AF026939	6	Pass	14.33	12.68	11	Pass	TRUE	FALSE	FALSE	5.18	2.77		10q24	
40955_at	UNK_U79	U79287	5	Pass	7.60	2.70	8	Pass	TRUE	FALSE	FALSE	2.75	2.76	prostate tumor over expressed gene 1; PTOV1		
35653_at	GPS2	U28963	6	Pass	24.00	6.39	13	Pass	TRUE	FALSE	FALSE	8.69	2.76	G protein pathway suppressor 2; GPS2		
181_g_at	UNK_S824	S82470	6	Pass	26.17	15.45	10	Pass	TRUE	FALSE	FALSE	9.50	2.75	BB1-malignant cell expression-enhanced gene/tumor progression-enhanced gene (human, UM-UC-9 bladder carcinoma cell line.		
38445_at	ARHGEF1	Y09160	6	Pass	24.33	6.77	13	Pass	TRUE	FALSE	FALSE	8.85	2.75	Rho guanine nucleotide exchange factor (GEF) 1; ARHGEF1	19q13.13	
37992_s_at	ATP5D	A1436567	6	Pass	34.83	13.91	13	Pass	TRUE	FALSE	FALSE	12.69	2.74	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit; ATP5D		

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36780_at	CLU	M25915	6	Pass	248.17	77.71	13	TRUE	FALSE	FALSE	90.46	clusterin (complement lysis inhibitor, SP-40), sulfated glycoprotein 2, testosterone-repressed prostate message 2	8p21-p12	
38798_s_at	GZAD	A1741833	6	Pass	16.67	3.27	13	TRUE	FALSE	FALSE	6.08	adaptor-related protein complex 1, gamma 2 subunit, APIG2		
35773_i_at	NDUFB7	AA527880	6	Pass	12.33	6.35	10	TRUE	FALSE	FALSE	4.50	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (18kD, B18); NDUFB7		
36979_at	SLC2A3	M20681	6	Pass	39.83	11.44	13	TRUE	FALSE	FALSE	14.54	solute carrier family 2 (facilitated glucose transporter), member 3; SLC2A3	12p13.3	
38517_at	ISGF3G	M87503	5	Pass	43.20	12.15	13	TRUE	FALSE	FALSE	15.77	interferon-stimulated transcription factor 3, gamma (48kD); ISGF3G	14q11.2	
41161_at	DAXX	AB015051	6	Pass	33.50	15.22	13	TRUE	FALSE	FALSE	12.23	death-associated protein 6; DAXX	6p21.3	
37591_at	UCP2	U94592	6	Pass	61.00	19.28	13	TRUE	FALSE	FALSE	22.31	uncoupling protein 2 (mitochondrial, proton carrier); UCP2	11q13	
38391_at	CAPG	M94345	6	Pass	37.00	18.49	13	TRUE	FALSE	FALSE	13.54	capping protein (actin filament), gelsolin-like; CAPG	2cen-q24	
33855_at	GRB2	M96995	6	Pass	16.17	6.97	13	TRUE	FALSE	FALSE	5.92	growth factor receptor-bound protein 2; GRB2	17q24-q25	
35626_at	SGSH	U30894	6	Pass	33.17	9.20	13	TRUE	FALSE	FALSE	12.15	N-sulfoglucosaminine sulfohydrolase (sulfamidase); SGSH	17q25.3	
33916_at	I-1	AB023192	6	Pass	23.00	9.14	9	TRUE	FALSE	FALSE	8.44	candidate; I-1	3p21.1	
37100_at	C17ORF1B	AJ008112	6	Pass	22.17	6.55	13	TRUE	FALSE	FALSE	8.15	chromosome 17 open reading frame 1B; C17ORF1B	17q21	
36554_at	ASMTL	Y15521	6	Pass	14.67	7.84	7	TRUE	FALSE	FALSE	5.43	acetylserotonin O-methyltransferase-like; ASMTL	Xp22.3, Yp11.3,	
31870_at	CD37	X14046	6	Pass	138.67	42.00	13	TRUE	FALSE	FALSE	51.38	CD37 antigen; CD37	19p13-q13.4	
41047_at	UNK_A188	A1885170	6	Pass	36.50	8.19	13	TRUE	FALSE	FALSE	13.54	immediate early protein; ETR101	19	
36097_at	ETR101	M62831	6	Pass	105.00	35.94	13	TRUE	FALSE	FALSE	39.00	transportin-SR; TRN-SR	7	
35813_at	TRN-SR	AA192359	6	Pass	15.17	8.38	11	TRUE	FALSE	FALSE	5.64	methyl-CpG binding domain protein 3; MBD3	19p13.3	
41160_at	UNK_AC0	AC005943	6	Pass	8.67	5.75	9	TRUE	FALSE	FALSE	3.22	SHC (Src homology 2 domain-containing) transforming protein 1; SHC1	1q21	
38118_at	SHC1	U73377	6	Pass	26.17	10.82	13	TRUE	FALSE	FALSE	9.77	solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; SLC25A1	22q11.21	
38997_at	SLC25A1	X96924	6	Pass	10.17	8.04	10	TRUE	FALSE	FALSE	3.80	interferon regulatory factor 3; IRF3	19q13.3-q13.4	
371_at	IRF3	Z56281	6	Pass	15.67	3.88	7	TRUE	FALSE	FALSE	5.86	peptidylprolyl isomerase B (cyclophilin B); PPIB	15q21-q22	
35823_at	PPIB	M63573	6	Pass	75.00	22.64	13	TRUE	FALSE	FALSE	28.08	RNA binding protein; AT-rich element binding factor; SRN300	16p13.3	
32761_at	KIAA0324	AB002322	6	Pass	35.33	7.58	13	TRUE	FALSE	FALSE	13.23			

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33908_at	CAPN1	X04366	6	Pass	56.50	21.92	13	Pass	TRUE	FALSE	21.23	2.66	calpain, large polypeptide 1; CAPN1	11q13		
38597_f_at	SLC11A1	D50402	4	Pass	9.50	4.12	7	Pass	TRUE	FALSE	3.57	2.66	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1; SLC11A1	2q35		
36675_r_at	PFN1	J03191	6	Pass	174.17	57.46	13	Pass	TRUE	FALSE	65.54	2.66	profilin 1; PFN1	17p13.3		
32836_at	AGPAT1	U56417	6	Pass	25.33	2.80	13	Pass	TRUE	FALSE	9.54	2.66	1-acylglycerol-3-phosphate O-acyltransferase 1	6p21.3		
38417_at	AMPD2	M91029	6	Pass	27.00	10.08	12	Pass	TRUE	FALSE	10.17	2.66	(lysophosphatidic acid acyltransferase, alpha); adenosine monophosphate deaminase 2 (isoform L); AMPD2	1p13.3		
39061_at	BST2	D28137	6	Pass	59.33	33.66	13	Pass	TRUE	FALSE	22.38	2.65	bone marrow stromal cell antigen 2; BST2	19p13.2		
38442_at	MFAP2	U19718	4	Pass	16.25	1.71	7	Pass	TRUE	FALSE	6.14	2.65	microfibrillar-associated protein 2; MFAP2	1p36.1-p35		
35629_at	UNK AL022238		6	Pass	23.00	12.21	11	Pass	TRUE	FALSE	8.73	2.64	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin); RNASE2	14q24-q31		
36766_at	RNASE2	X55988	6	Pass	37.50	29.43	13	Pass	TRUE	FALSE	14.23	2.64	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin); RNASE2	14q24-q31		
34670_at	MAN2B1	U60899	6	Pass	31.00	10.68	13	Pass	TRUE	FALSE	11.77	2.63	mannosidase, alpha, class 2B, member 1; MAN2B1	19cen-q13.1		
41164_at	IGHM	X67301	6	Pass	134.17	51.81	13	Pass	TRUE	FALSE	51.00	2.63	immunoglobulin heavy constant mu; IGHM	14q32.33		
1693_s_at	TIMP1	D11139	6	Pass	51.50	23.10	13	Pass	TRUE	FALSE	19.62	2.63	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor); TIMP1	Xp11.3-p11.23		
36661_s_at	CD14	X06882	6	Pass	156.17	111.56	13	Pass	TRUE	FALSE	59.54	2.62	CD14 antigen; CD14	5q31.1		
37386_i_at	KDELR1	X55885	6	Pass	38.50	24.19	13	Pass	TRUE	FALSE	14.69	2.62	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1; KDELR1	19q13.3		
39358_at	NCOR2	U37146	6	Pass	22.17	10.13	13	Pass	TRUE	FALSE	8.46	2.62	nuclear receptor co-repressor 2; NCOR2	12q24		
31431_at	FCGRT	U12255	6	Pass	32.83	18.49	13	Pass	TRUE	FALSE	12.54	2.62	Fc fragment of IgG, receptor, transporter, alpha; FCGRT	19q13.3		
40725_at	GOSR1	AF047438	6	Pass	9.67	4.27	13	Pass	TRUE	FALSE	3.69	2.62	golgi SNAP receptor complex member 1; GOSR1	17q11		
1754_at	DAXX	AF006041	6	Pass	14.83	4.92	12	Pass	TRUE	FALSE	5.67	2.62	death-associated protein 6; DAXX	6p21.3		
37179_at	NFE2	S77763	6	Pass	15.50	8.02	13	Pass	TRUE	FALSE	5.92	2.62	nuclear factor (erythroid-derived 2), 45kD; NFE2	12q13		
1067_at	FLT3LG	U03858	6	Pass	8.50	1.87	12	Pass	TRUE	FALSE	3.25	2.62	fms-related tyrosine kinase 3 ligand; FLT3LG	19q13.3		
38547_at	ITGAL	Y00796	6	Pass	29.33	7.63	13	Pass	TRUE	FALSE	11.23	2.61	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide); ITGAL	16p11.2		
38730_at	KIAA0864	AB020671	6	Pass	22.50	3.94	13	Pass	TRUE	FALSE	8.62	2.61	KIAA0864 protein;			
33841_at	EIF5	R48209	6	Pass	10.83	3.87	12	Pass	TRUE	FALSE	4.17	2.60	kinesin-like 5 (mitotic kinesin-like protein 1); KNSL5			

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503_at	POLR2L	U37690	5	Pass	41.60	10.53	13	Pass	TRUE	FALSE	16.00	2.60	polymerase (RNA) II (DNA directed) polypeptide L (7.6kD); POLR2L	11p15
39050_at	PABPN1	AF026029	6	Pass	24.00	7.40	13	Pass	TRUE	FALSE	9.23	2.60	poly(A)-binding protein, nuclear I; PABPN1	14q11.2- q13
947_at	MCM7	D55716	6	Pass	11.17	4.22	10	Pass	TRUE	FALSE	4.30	2.60	minichromosome maintenance deficient (S. cerevisiae) 7; MCM7	7q21.3- q22.1
33836_at	NPIP	AC002045	6	Pass	12.33	2.25	8	Pass	TRUE	FALSE	4.75	2.60	nuclear pore complex interacting protein; NPIP	16p13- p11
39910_at	UNK_AA6	AA663800	6	Pass	10.17	2.64	13	Pass	TRUE	FALSE	3.92	2.59	hypothetical protein; LOC51257	
32091_at	UNK_AB0	AB007915	6	Pass	11.00	6.72	12	Pass	TRUE	FALSE	4.25	2.59	KIAA0446 gene product; KIAA0446	1
1131_at	MAP2K2	L11285	6	Pass	24.83	5.19	13	Pass	TRUE	FALSE	9.62	2.58	mitogen-activated protein kinase kinase 2; MAP2K2	7q32
40448_at	ZFP36	M92843	6	Pass	43.83	24.09	13	Pass	TRUE	FALSE	17.00	2.58	zinc finger protein homologous to Zfp-36 in mouse; ZFP36	19q13.1
39280_at	TNRC5	U80744	6	Pass	10.50	5.32	11	Pass	TRUE	FALSE	4.09	2.57	trinucleotide repeat containing 5; TNRC5	1
35674_at	PD12	AB023211	4	Pass	10.25	6.13	7	Pass	TRUE	FALSE	4.00	2.56	peptidyl arginine deiminase, type II; PD12	
198_g_at	NME3	U29656	6	Pass	22.83	6.65	13	Pass	TRUE	FALSE	8.92	2.56	non-metastatic cells 3; protein expressed in; NME3	16q13
31812_at	GMPR	M24470	6	Pass	19.17	7.63	12	Pass	TRUE	FALSE	7.50	2.56	guanosine monophosphate reductase; GMPR	6p23
40296_at	UNK_AL0	AL023653	6	Pass	29.83	11.79	13	Pass	TRUE	FALSE	11.69	2.55	aminolevulinic, delta- synthase 2	Xp11.21
37285_at	ALAS2	X60364	6	Pass	84.33	43.66	13	Pass	TRUE	FALSE	33.08	2.55	{sideroblastic/hypochromic anemia}; ALAS2	
36994_at	ATP6C	M62762	6	Pass	60.17	24.26	13	Pass	TRUE	FALSE	23.62	2.55	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD;	16p13.3
34532_at	UNK_AF0	AF035318	6	Pass	16.67	6.74	11	Pass	TRUE	FALSE	6.55	2.55	KIAA0779 protein;	
33251_at	KIAA0779	AB018322	6	Pass	6.50	1.76	9	Pass	TRUE	FALSE	2.56	2.54	KIAA0779	
33860_at	KIAA0462	AB007931	6	Pass	21.67	6.28	13	Pass	TRUE	FALSE	8.54	2.54	KIAA0462 protein;	1
39437_at	UNK_Z78	Z78324	6	Pass	18.33	7.20	13	Pass	TRUE	FALSE	7.23	2.54	SH3 domain-containing protein 6511; LOC51165	
39601_at	RDA32	AF061836	6	Pass	26.50	6.77	13	Pass	TRUE	FALSE	10.46	2.53	Ras association (RalGDS/AF-6) domain family 1; RASSF1	3p21.3
32773_at	HLA-DQA	AA868382	6	Pass	57.83	23.45	13	Pass	TRUE	FALSE	22.92	2.52	major histocompatibility complex, class II, DQ alpha 1; HLA-DQA1	6p21.3
33398_at	KIAA0670	AB014570	6	Pass	29.67	13.52	9	Pass	TRUE	FALSE	11.78	2.52	KIAA0670 protein/actin; KIAA0670	14
31622_f_at	MT1F	M10943	5	Pass	29.00	15.70	11	Pass	TRUE	FALSE	11.55	2.51	metallothionein 1F (functional); MT1F	16q13
36678_at	TAGLN2	D21261	6	Pass	175.00	42.08	13	Pass	TRUE	FALSE	69.69	2.51	transgelin 2; TAGLN2	1q21-q25
33659_at	CFL1	X95404	6	Pass	207.83	56.94	13	Pass	TRUE	FALSE	82.92	2.51	cofilin 1 (non-muscle); CFL1	11q13
497_at	CLN3	U32680	6	Pass	18.00	5.80	11	Pass	TRUE	FALSE	7.18	2.51	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeier-Vogt disease); CLN3	16p12.1

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39704_g_at	HMG1Y	L17131	5	Pass	20.40	4.77	7	Pass	TRUE	FALSE	FALSE	8.14	high-mobility group (nonhistone chromosomal) protein isoforms I and Y; HMG1Y	6p21	*
31432_g_at	FCGRT	U12255	6	Pass	57.33	28.74	12	Pass	TRUE	FALSE	FALSE	22.92	Fc fragment of IgG. receptor, transporter.	19q13.3	
31915_s_at	UNK_U75	U75968	5	Pass	17.20	5.07	8	Pass	TRUE	FALSE	FALSE	6.88	alpha-FCGRT DEAD/H (Asp-Glu-Ala- Asp/His) box polypeptide 11 (S.cerevisiae CHL1- like helicase); DDX11	12p11	
35965_at	HSPA6	X51757	6	Pass	14.17	8.91	9	Pass	TRUE	FALSE	FALSE	5.67	heat shock 70kD protein 6 (HSP70B); HSPA6	1cen-qter	
40867_at	PPP2R1A	J02902	5	Pass	30.40	5.94	12	Pass	TRUE	FALSE	FALSE	12.17	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform; PPP2R1A		
32824_at	CLN2	AF039704	6	Pass	37.83	17.23	13	Pass	TRUE	FALSE	FALSE	15.15	ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease); CLN2	11p15	
40098_at	EHD1	AF001434	6	Pass	18.50	3.21	12	Pass	TRUE	FALSE	FALSE	7.42	EH domain containing 1; EHD1	11q13	
879_at	MX2	M30818	6	Pass	16.50	9.14	13	Pass	TRUE	FALSE	FALSE	6.62	myxovirus (influenza) resistance 2, homolog of murine; MX2	21q22.3	
1790_s_at	CDK10	X78342	6	Pass	18.50	6.16	7	Pass	TRUE	FALSE	FALSE	7.43	cyclin-dependent kinase (CDC2-like) 10; CDK10	16q24	
411_i_at	IFITM2	X57351	6	Pass	51.67	27.91	13	Pass	TRUE	FALSE	FALSE	20.77	interferon induced transmembrane protein 2		
915_at	IFIT1	M24594	4	Pass	9.25	3.30	11	Pass	TRUE	FALSE	FALSE	3.73	interferon-induced protein (1-8D); IFITM2	10q25- q26	
38361_g_at	RASGRP2	A1688812	6	Pass	14.50	0.84	13	Pass	TRUE	FALSE	FALSE	5.85	RAS guanyl releasing protein 2 (calcium and DAG-regulated); RASGRP2	11q13	
38631_at	TNFAIP2	M92357	6	Pass	43.83	20.08	13	Pass	TRUE	FALSE	FALSE	17.69	tumor necrosis factor, alpha-induced protein 2; TNFAIP2	14q32	
33207_at	PRKRI	A1095508	6	Pass	9.17	4.54	10	Pass	TRUE	FALSE	FALSE	3.70	protein-kinase, interferon- inducible double stranded RNA dependent inhibitor; PRKRI	13q32	
31673_s_at	CMAR	X65784	6	Pass	20.00	5.93	13	Pass	TRUE	FALSE	FALSE	8.08	cell matrix adhesion regulator,spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive); CMAR	16q16q24 .3	
40099_at	LFP40	AB014551	6	Pass	20.00	10.20	13	Pass	TRUE	FALSE	FALSE	8.08	rho/rac guanine nucleotide exchange factor (GEF) 2; ARHGEF2	1	
34206_at	KIAA0782	AB018325	6	Pass	20.17	8.66	13	Pass	TRUE	FALSE	FALSE	8.15	KIAA0782 protein; KIAA0782		
329_s_at	NUMA1	Z11584	6	Pass	18.83	5.27	13	Pass	TRUE	FALSE	FALSE	7.62	nuclear mitotic apparatus protein 1; NUMA1	11q13	
36447_at	FCN1	S80990	6	Pass	246.17	113.27	13	Pass	TRUE	FALSE	FALSE	99.69	ficollin (collagen/fibrinogen domain-containing) 1; FCN1	9q34	
41222_at	STAT6	AF067575	6	Pass	55.83	30.42	13	Pass	TRUE	FALSE	FALSE	22.62	signal transducer and activator of transcription 6; interleukin-4 induced; STAT6	12q13	*

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35094_f_at	LILRA3	AF025527	6	Pass	26.00	15.35	12	Pass	TRUE	FALSE	FALSE	10.58	2.46	leukocyte immunoglobulin like receptor, subfamily A (without TM domain), member 3; LILRA3	19q13.4	
33453_at	ATP6S1	A1400326	6	Pass	51.00	12.95	13	Pass	TRUE	FALSE	FALSE	20.77	2.46	ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), subunit I;	Xq28	
41409_at	ICB-1	AF044896	6	Pass	44.67	23.90	13	Pass	TRUE	FALSE	FALSE	18.23	2.45	basement membrane- induced gene; ICB-1		
33887_at	HGS	D84064	6	Pass	16.83	3.66	8	Pass	TRUE	FALSE	FALSE	6.88	2.45	human growth factor- regulated tyrosine kinase substrate; HGS	17q25	
36936_at	TSTA3	U58766	6	Pass	10.17	1.60	13	Pass	TRUE	FALSE	FALSE	4.15	2.45	tissue specific transplantation antigen P35B; TSTA3	8q24.3	
117_at	HSPA6	X51757	5	Pass	10.40	4.22	8	Pass	TRUE	FALSE	FALSE	4.25	2.45	heat shock 70kD protein 6 (HSP70B); HSPA6	1cen-qter	
32211_at	PSMD13	AB009398	6	Pass	10.83	7.28	7	Pass	TRUE	FALSE	FALSE	4.43	2.45	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13; PSMD13	11p15.5	
41337_at	AES	AF072902	6	Pass	49.67	16.39	13	Pass	TRUE	FALSE	FALSE	20.31	2.45	amino-terminal enhancer of split; AES	19p13.3	
33230_at	NMFP200	AJ131186	6	Pass	14.67	4.03	12	Pass	TRUE	FALSE	FALSE	6.00	2.44	nuclear matrix protein NMFP200 related to splicing factor PRP19;	11q12.2	
39062_at	PPGB	AL008726	6	Pass	53.17	15.46	13	Pass	TRUE	FALSE	FALSE	21.77	2.44	protective protein for beta- galactosidase (galactosialidosis); PPCB	20q13.1	
40609_at	UNK_A141	A1475497	6	Pass	10.50	3.45	10	Pass	TRUE	FALSE	FALSE	4.30	2.44	RAS guanyl releasing protein 2 (calcium and DAG-regulated); RASGRP2	11q13	
38359_at	RASGRP2	Y12336	6	Pass	54.67	8.16	13	Pass	TRUE	FALSE	FALSE	22.46	2.43	cytochrome b-245, alpha polypeptide; CYBA	16q24	
35807_at	CYBA	M21186	6	Pass	218.67	86.22	13	Pass	TRUE	FALSE	FALSE	89.92	2.43	small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen); SNRP70	19q13.3	
40875_s_at	SNRP70	X06815	6	Pass	75.00	22.68	13	Pass	TRUE	FALSE	FALSE	30.85	2.43	protein kinase C substrate 80K-H; PRKCSH	19p13.1- p13.2	
39711_at	PRKCSH	J03075	6	Pass	18.50	5.09	13	Pass	TRUE	FALSE	FALSE	7.62	2.43	arsenate resistance protein 7421	7q21	
39832_at	LOC51593	AL096723	6	Pass	12.33	3.61	12	Pass	TRUE	FALSE	FALSE	5.08	2.43	ARS2; LOC51593		
40160_at	DKFZP586	AL080109	6	Pass	15.67	4.46	13	Pass	TRUE	FALSE	FALSE	6.46	2.42	DKFZP586P2220 protein;		
39823_at	H326	U06631	5	Pass	20.40	5.32	12	Pass	TRUE	FALSE	FALSE	8.42	2.42	H326; H326		
37351_at	UP	X90858	6	Pass	21.00	11.92	12	Pass	TRUE	FALSE	FALSE	8.67	2.42	uridine phosphorylase; UP	7	
35566_f_at	UNK_AF0	AF015128	6	Pass	30.00	20.82	13	Pass	TRUE	FALSE	FALSE	12.38	2.42	zinc finger protein 151 (pH2-67); ZNF151	1p36.2- p36.1	
41532_at	ZNF151	Y09723	6	Pass	8.17	2.40	8	Pass	TRUE	FALSE	FALSE	3.38	2.42	KIAA0542 gene product; KIAA0542	22q12.2	
36545_s_at	UNK_AB0	AB011114	6	Pass	11.17	3.31	13	Pass	TRUE	FALSE	FALSE	4.62	2.42	phosphatidylinositol transfer protein, membrane associated; PTPNM	11q13	
38297_at	PTPNM	X98654	6	Pass	53.00	15.01	13	Pass	TRUE	FALSE	FALSE	21.92	2.42	natural killer cell group 7 sequence; NKG7	19	
37121_at	NKG7	S69115	6	Pass	95.67	55.68	13	Pass	TRUE	FALSE	FALSE	39.62	2.41	glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II); GAA	17q25.2- q25.3	
31816_at	GAA	X55079	6	Pass	18.00	9.32	11	Pass	TRUE	FALSE	FALSE	7.45	2.41			

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38029_at	MDU1	J02939	6	Pass	19.67	5.92	13	Pass	FALSE	FALSE	8.15	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2; SLC3A2	11q13	
32550_r_at	CEBPA	Y11525	6	Pass	27.00	10.02	10	Pass	FALSE	FALSE	11.20	CCAAT/enhancer binding protein (C/EBP), alpha; CEBPA	19q13.1	
33613_at	UNK_AAB	AA806239	5	Pass	8.60	1.52	7	Pass	FALSE	FALSE	3.57	paired mesoderm homeobox 1; PMX1	1q24	
40127_at	PMX1	M95929	6	Pass	16.67	5.20	13	Pass	FALSE	FALSE	6.92	expressed in activated T/LAK lymphocytes; LAK 4P	17q25	
32116_at	UNK_AB0	AB002405	6	Pass	38.50	8.89	13	Pass	FALSE	FALSE	16.00	KIAA0618 gene product, hypothetical protein FLJ10267; FLJ10267.KIAA0618		
41258_at	KIAA0618	N29665	6	Pass	35.50	6.25	13	Pass	FALSE	FALSE	14.77	keratin 1 (epidermolytic hyperkeratosis); KRT1	12q11-q13	
558_at	KRT1	M98776	5	Pass	12.20	5.26	13	Pass	FALSE	FALSE	5.08	valyl-tRNA synthetase 2; VARS2	6p21.3	
40414_at	VARS2	X59303	6	Pass	20.33	4.46	13	Pass	FALSE	FALSE	8.46	KIAA0088 protein; KIAA0088		
956_at	TUBB	X79535	6	Pass	23.00	7.13	7	Pass	FALSE	FALSE	9.57	adaptor-related protein complex 2, beta 1 subunit; AP2B1	17q11.2-q12	
37040_at	KIAA0088	D42041	6	Pass	37.50	11.67	13	Pass	FALSE	FALSE	15.62	interferon-induced protein 35; IFI35	17q21	
36161_at	ADTB2	M34175	6	Pass	18.83	7.94	13	Pass	FALSE	FALSE	7.85	ins-related tyrosine kinase 3 ligand; FLT3LG	19q13.3	
626_s_at	IFI35	L78833	5	Pass	5.40	4.04	8	Pass	FALSE	FALSE	2.25	DKFZP586J2223 protein; DKFZP586J2223		
36314_at	FLT3LG	U04806	6	Pass	13.50	3.67	11	Pass	FALSE	FALSE	5.64	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin); SPTAN1	9q33-q34	
36030_at	DKFZP586	AL080214	6	Pass	21.00	6.13	13	Pass	FALSE	FALSE	8.77	tumor necrosis factor receptor superfamily, member 1B; TNFRSF1B	1p36.3-p36.2	
33833_at	SPTAN1	J05243	6	Pass	13.17	2.64	10	Pass	FALSE	FALSE	5.50	HSA011916	17p13	
33813_at	TNFRSF1B	A1813532	6	Pass	167.50	76.07	13	Pass	FALSE	FALSE	70.08	lectin, galactoside-binding, soluble, 1 (galectin 1); LGALS1	22q13.1	
38483_at	HSA01191	AJ011916	6	Pass	37.50	15.98	13	Pass	FALSE	FALSE	15.69	solute carrier family 31 (copper transporters), member 2; SLC31A2	9q31-q32	
33412_at	LGALS1	A1535946	6	Pass	99.50	46.06	13	Pass	FALSE	FALSE	41.77	KIAA0342 gene product; KIAA0342		
34749_at	SLC31A2	U83461	5	Pass	18.40	8.65	11	Pass	FALSE	FALSE	7.73	guanylate kinase 1; GUK1	1q32-q41	
32660_at	UNK_AB0	AB002340	6	Pass	16.67	4.23	10	Pass	FALSE	FALSE	7.00	myeloid cell leukemia sequence 1 (BCL2-related); MCL1	1q21	
905_at	GUK1	L76200	6	Pass	46.33	17.22	13	Pass	FALSE	FALSE	19.46	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform; PPP2R1A		
277_at	MCL1	L08246	6	Pass	115.17	44.97	13	Pass	FALSE	FALSE	48.38	docking protein 1, 62kD (downstream of tyrosine kinase 1); DOK1	2p13	
922_at	PPP2R1A	J02902	6	Pass	33.50	8.36	13	Pass	FALSE	FALSE	14.08	small inducible cytokine A5 (RANTES); SCYA5	17q11.2-q12	
34433_at	DOK1	AF035299	6	Pass	20.33	17.93	11	Pass	FALSE	FALSE	8.55			
1403_s_at	SCYA5	M21121	6	Pass	181.00	62.86	13	Pass	FALSE	FALSE	76.15			

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37026_at	COPEB	AF001461	6	Pass	26.50	13.94	13	Pass	TRUE	FALSE	FALSE	11.15	2.38	core promoter element binding protein; COPEB	10p15	
1997_s_at	BAX	U19599	6	Pass	11.83	5.04	11	Pass	TRUE	FALSE	FALSE	5.00	2.37	BCL2-associated X protein; BAX	19q13.3-q13.4	
33866_at	TPM4	X05276	6	Pass	7.33	1.63	10	Pass	TRUE	FALSE	FALSE	3.10	2.37	tropomyosin 4; TPM4	19p13.1	
38051_at	MAL	X76220	6	Pass	31.83	15.48	13	Pass	TRUE	FALSE	FALSE	13.46	2.36	mal, T-cell differentiation protein; MAL	2cen-q13	
1347_at	CDC25B	S78187	6	Pass	33.83	10.44	13	Pass	TRUE	FALSE	FALSE	14.31	2.36	cell division cycle 25B; CDC25B	20p13	
36603_at	GCN1L1	D86973	6	Pass	14.00	2.61	13	Pass	TRUE	FALSE	FALSE	5.92	2.36	GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; GCN1L1	12q24.2	
36058_at	DKFZP580AL09741		6	Pass	14.33	2.42	13	Pass	TRUE	FALSE	FALSE	6.08	2.36	hypothetical protein; DKFZP580O0223	22	
40196_at	HYA22	D88153	5	Pass	10.40	3.65	12	Pass	TRUE	FALSE	FALSE	4.42	2.35	HYA22 protein; HYA22	3p21.3	
33361_at	GNG3LG	AF052149	6	Pass	14.67	2.66	13	Pass	TRUE	FALSE	FALSE	6.23	2.35	guanine nucleotide binding protein (G protein), gamma 3, linked;	11q12-q13.5	
34491_at	OASL	AJ225089	6	Pass	7.33	5.39	8	Pass	TRUE	FALSE	FALSE	3.13	2.35	2'-5'-oligoadenylate synthetase-like; OASL	12q24.2	
41165_g_at	IGHM	X67301	6	Pass	150.00	56.88	13	Pass	TRUE	FALSE	FALSE	63.92	2.35	immunoglobulin heavy constant mu; IGHM	14q32.33	
31504_at	HDLBP	M64098	6	Pass	13.67	4.68	12	Pass	TRUE	FALSE	FALSE	5.83	2.34	high density lipoprotein binding protein (vigilin); HDLBP	2q37	
1237_at	IER3	S81914	5	Pass	10.40	5.32	9	Pass	TRUE	FALSE	FALSE	4.44	2.34	immediate early response 3; IER3	6p21.3	
38117_at	SEC24C	D38555	6	Pass	15.67	3.44	10	Pass	TRUE	FALSE	FALSE	6.70	2.34	SEC24 (S. cerevisiae) related gene family, member C; SEC24C	10	
38423_at	UNK_L38	L38935	6	Pass	36.50	12.47	13	Pass	TRUE	FALSE	FALSE	15.62	2.34			
38064_at	LRP	X79882	6	Pass	23.17	10.70	13	Pass	TRUE	FALSE	FALSE	9.92	2.33	major vault protein; MVP	16p13.1-p11.2	
39158_at	ATF5	AB021663	6	Pass	7.00	3.58	10	Pass	TRUE	FALSE	FALSE	3.00	2.33	activating transcription factor 5; ATF5		
39597_at	KIAA0843	AB020650	6	Pass	10.50	4.97	12	Pass	TRUE	FALSE	FALSE	4.50	2.33	KIAA0843 protein;		
34695_at	GA17	A1816724	6	Pass	30.67	18.23	13	Pass	TRUE	FALSE	FALSE	13.15	2.33	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2; SMARCD2	17q23-q24	
39994_at	CCR1	D10925	5	Pass	17.60	14.91	9	Pass	TRUE	FALSE	FALSE	7.56	2.33	chemokine (C-C motif) receptor 1; CCR1	3p21	
37799_at	ASGR2	X55284	6	Pass	13.33	6.31	11	Pass	TRUE	FALSE	FALSE	5.73	2.33	asialoglycoprotein receptor 2; ASGR2	17p	
496_s_at	IL11RA	U22324	6	Pass	9.67	3.20	13	Pass	TRUE	FALSE	FALSE	4.15	2.33	interleukin 11 receptor, alpha; IL11RA	9p13	
849_g_at	UNK_U19	U19261	6	Pass	10.00	2.45	13	Pass	TRUE	FALSE	FALSE	4.31	2.32	TNF receptor-associated factor 1; TRAF1	9q33-q34	
34691_t_at	ARPC4	AF006087	6	Pass	25.00	6.63	13	Pass	TRUE	FALSE	FALSE	10.77	2.32	actin related protein 2/3 complex, subunit 4 (20 kD); ARPC4		
35244_at	KIAA0460	AB007929	5	Pass	11.60	3.65	11	Pass	TRUE	FALSE	FALSE	5.00	2.32	KIAA0460 protein;	1	
32336_at	ALDOA	X05236	6	Pass	129.33	37.93	13	Pass	TRUE	FALSE	FALSE	55.77	2.32	aldolase A, fructose-bisphosphate; ALDOA	16q22-q24	
33838_at	D6S52E	M33519	6	Pass	30.67	4.37	13	Pass	TRUE	FALSE	FALSE	13.23	2.32	HLA-B associated transcript-3; D6S52E	6p21.3	
40885_s_at	UNK_N30	N30151	6	Pass	18.33	2.58	13	Pass	TRUE	FALSE	FALSE	7.92	2.31	eukaryotic translation initiation factor 4B; EIF4B		
38893_at	NCF4	AL008637	6	Pass	55.17	27.67	13	Pass	TRUE	FALSE	FALSE	23.85	2.31	neutrophil cytosolic factor 4 (40kD); NCF4	22q13.1	

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40365_at	GNAI5	M63904	6	Pass	15.83	7.47	13	Pass	TRUE	FALSE	FALSE	6.85	2.31	guanine nucleotide binding protein (G protein), alpha 15 (Gq class); GNAI5	19p13.3	
39795_at	CLAPM1	D63475	6	Pass	80.00	25.55	13	Pass	TRUE	FALSE	FALSE	34.62	2.31	adaptor-related protein complex 2, mu 1 subunit; AP2M1	3q28	
38729_at	FKBP4	M88279	6	Pass	11.17	3.06	12	Pass	TRUE	FALSE	FALSE	4.83	2.31	FK506-binding protein 4 (59kD); FKBP4		
39385_at	ANPEP	M22324	6	Pass	16.50	5.75	7	Pass	TRUE	FALSE	FALSE	7.14	2.31	blanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150); ANPEP	15q25-q26	
37298_at	GABARAP	AF044671	6	Pass	123.67	48.80	13	Pass	TRUE	FALSE	FALSE	53.54	2.31	GABA(A) receptor-associated protein; GABARAP	17	
2019_s_at	ITGB7	M68892	6	Pass	13.50	6.35	13	Pass	TRUE	FALSE	FALSE	5.85	2.31	integrin, beta 7; ITGB7	12q13.13	
36035_at	GPAAL	AB002135	6	Pass	24.33	6.83	13	Pass	TRUE	FALSE	FALSE	10.54	2.31	glycophosphatidylinositol anchor attachment 1; GPAAL	8q24.3	
37796_at	UNK_AFO	AF053156	6	Pass	28.33	2.94	11	Pass	TRUE	FALSE	FALSE	12.27	2.31	leucine-rich neuronal protein; LRN	7q22	
32174_at	SLC9A3R1	AF015926	6	Pass	29.83	5.27	13	Pass	TRUE	FALSE	FALSE	12.92	2.31	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1; SLC9A3R1		
36322_at	FUT7	AB012668	4	Pass	10.00	3.46	9	Pass	TRUE	FALSE	FALSE	4.33	2.31	fucosyltransferase 7 (alpha 9) (1.3) fucosyltransferase); FUT7		
38091_at	LGALS9	Z49107	6	Pass	60.00	23.87	13	Pass	TRUE	FALSE	FALSE	26.00	2.31	lectin, galactoside-binding, soluble, 9 (galectin 9); LGALS9		
33706_at	SART1	AB006198	6	Pass	19.50	4.72	13	Pass	TRUE	FALSE	FALSE	8.46	2.30	squamous cell carcinoma antigen recognised by T cells; SART1		
1919_at	VAV1	X16316	4	Pass	13.25	3.77	8	Pass	TRUE	FALSE	FALSE	5.75	2.30	vav 1 oncogene; VAV1	19p13.2	
39033_at	HPRP3P	AF016370	6	Pass	6.33	1.63	8	Pass	TRUE	FALSE	FALSE	2.75	2.30	U4/U6-associated RNA splicing factor; HPRP3P	1q21.1	
880_at	FKBP1A	M34539	6	Pass	59.33	20.33	13	Pass	TRUE	FALSE	FALSE	25.77	2.30	FK506-binding protein 1A (12kD); FKBP1A	20p13	
37947_at	KIAA0043	D26362	6	Pass	16.50	8.46	12	Pass	TRUE	FALSE	FALSE	7.17	2.30	KIAA0043 gene product; KIAA0043		
37376_at	LOC51035	M68864	6	Pass	28.33	9.73	13	Pass	TRUE	FALSE	FALSE	12.31	2.30	ORF; LOC51035		
32218_at	UNK_AFO	AF034176	6	Pass	31.67	11.67	13	Pass	TRUE	FALSE	FALSE	13.77	2.30			
41460_at	SIP	AF080561	6	Pass	9.00	3.95	12	Pass	TRUE	FALSE	FALSE	3.92	2.30	SYT interacting protein; SIP		
35749_at	TADA3L	AF069733	6	Pass	44.00	13.48	13	Pass	TRUE	FALSE	FALSE	19.15	2.30	transcriptional adaptor 3 (ADA3, yeast homolog)-like (PCAF histone acetylase complex); TADA3L		
38710_at	UNK_ALO	AL096714	6	Pass	29.67	8.82	13	Pass	TRUE	FALSE	FALSE	12.92	2.30	hypothetical protein FLJ20113; FLJ20113		
41386_i_at	KIAA0346	AB002344	6	Pass	16.83	5.60	12	Pass	TRUE	FALSE	FALSE	7.33	2.30	KIAA0346 protein; KIAA0346	17p13.1	
344_s_at	CNP	D13146	5	Pass	22.60	8.26	13	Pass	TRUE	FALSE	FALSE	9.85	2.30			
36162_at	BSG	X64364	6	Pass	18.00	2.28	13	Pass	TRUE	FALSE	FALSE	7.85	2.29	basigin; BSG	19p13.3	
36937_s_at	CLIM1	U90878	6	Pass	18.17	6.40	13	Pass	TRUE	FALSE	FALSE	7.92	2.29	carboxy terminal LIM domain protein 1; CLIM1	10qter	

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Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Fold Change (Normal) RA / Normal	Name	Chromosome	Phosphatase
1158_s_at	CALM3	J04046	6	Pass	22.50	4.04	11	Pass	TRUE	FALSE	FALSE	9.82	calmodulin 3 (phosphorylase kinase, delta); CALM3	19q13.2-q13.3	
38976_at	CORO1A	D44497	6	Pass	230.67	59.84	13	Pass	TRUE	FALSE	FALSE	100.77	coronin, actin-binding protein, 1A; CORO1A		
39722_at	NCOR1	AF044209	6	Pass	17.17	8.80	10	Pass	TRUE	FALSE	FALSE	7.50	nuclear receptor co-repressor 1; NCOR1	17p11.2	
32909_at	AQP5	U46569	6	Pass	11.67	3.50	10	Pass	TRUE	FALSE	FALSE	5.10	aquaporin 5; AQP5	12q13	
932_i_at	ZNF91	L11672	6	Pass	19.17	9.22	13	Pass	TRUE	FALSE	FALSE	8.38	zinc finger protein 91 (HPF7, HTF10); ZNF91	19p13.1-p12	
39908_at	PAF65A	AF069735	6	Pass	111.50	49.03	9	Pass	TRUE	FALSE	FALSE	48.78	PCAF associated factor 65 alpha; PAF65A		
31638_at	NDUFS7	AC005329	6	Pass	20.00	8.15	8	Pass	TRUE	FALSE	FALSE	8.75			
31137_at	LTBP4	Y13622	6	Pass	12.00	2.90	12	Pass	TRUE	FALSE	FALSE	5.25	latent transforming growth factor beta binding protein 4; LTBP4	19q13.1-q13.2	
39343_at	HSU53209	AW026656	6	Pass	7.17	4.12	7	Pass	TRUE	FALSE	FALSE	3.14	transformer-2 alpha (htra-2 alpha); HSU53209		
32370_at	GZMB	M57888	6	Pass	46.83	29.69	13	Pass	TRUE	FALSE	FALSE	20.54	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1); GZMB	14q11.2	
816_g_at	DOK1	U70987	6	Pass	30.17	18.29	13	Pass	TRUE	FALSE	FALSE	13.23	docking protein 1, 62kD (downstream of tyrosine kinase 1); DOK1	2p13	
32658_at	UNK_AL0	AL031228	6	Pass	10.33	2.25	13	Pass	TRUE	FALSE	FALSE	4.54			
36208_at	FSRG1	D42040	6	Pass	20.83	4.36	13	Pass	TRUE	FALSE	FALSE	9.15	bronodomain-containing 2; BRD2	6p21.3	
38998_g_at	SLC25A1	X96924	6	Pass	11.83	3.82	10	Pass	TRUE	FALSE	FALSE	5.20	solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; SLC25A1	22q11.21	
33146_at	MCL1	L08246	6	Pass	116.17	36.29	13	Pass	TRUE	FALSE	FALSE	51.08	myeloid cell leukemia sequence 1 (BCL2-related); MCL1	1q21	
402_s_at	ICAM3	X69819	6	Pass	46.33	18.16	13	Pass	TRUE	FALSE	FALSE	20.38	intercellular adhesion molecule 3; ICAM3	19p13.3-p13.2	
39971_at	LYL1	M22637	6	Pass	13.83	3.54	11	Pass	TRUE	FALSE	FALSE	6.09	lymphoblastic leukemia derived sequence 1; LYL1	19p13.2	
32646_at	KIAA0449	AB007918	5	Pass	22.20	3.56	9	Pass	TRUE	FALSE	FALSE	9.78	KIAA0449 protein; KIAA0449	1	
31901_at	KCNAB2	AF044253	6	Pass	28.50	8.12	9	Pass	TRUE	FALSE	FALSE	12.56	potassium voltage-gated channel, shaker-related subfamily, beta member 2; KCNAB2	1p36.3	
40147_at	VAT1	U18009	6	Pass	14.83	5.74	13	Pass	TRUE	FALSE	FALSE	6.54	membrane protein of cholinergic synaptic vesicles; VAT1	17q21	
40130_at	FSTL1	U06863	6	Pass	17.00	5.66	12	Pass	TRUE	FALSE	FALSE	7.50	folliculin-like 1; FSTL1	7q21.2-q31.1	
151_s_at	UNK_V00	V00599	6	Pass	42.17	11.99	13	Pass	TRUE	FALSE	FALSE	18.62	tubulin, beta polypeptide; TUBB	6p21.3	
766_at	LGALS9	AB006782	6	Pass	31.33	14.72	13	Pass	TRUE	FALSE	FALSE	13.85	lectin, galactoside-binding, soluble, 9 (galectin 9); LGALS9		
33863_at	ORP150	U65785	6	Pass	25.50	5.61	11	Pass	TRUE	FALSE	FALSE	11.27	oxygen regulated protein (150kD); ORP150	11	
41728_at	KIAA0152	D63486	6	Pass	19.83	5.00	13	Pass	TRUE	FALSE	FALSE	8.77	KIAA0152 gene product; KIAA0152	12	
37307_at	GNAI2	X04828	6	Pass	147.67	57.65	13	Pass	TRUE	FALSE	FALSE	65.31	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2; GNAI2	3p21	

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33826_at	CIZ1	AL120500	6	Pass	21.83	3.97	12	Pass	TRUE	FALSE	FALSE	9.67	Cip1-interacting zinc finger protein; CIZ1		9q34.1	
1795_g_at	CCND3	M92287	6	Pass	94.50	24.91	13	Pass	TRUE	FALSE	FALSE	41.85	cyclin D3; CCND3		6p21	
38674_at	IGFBP6	AA115140	6	Pass	103.50	49.49	13	Pass	TRUE	FALSE	FALSE	45.85	hypothetical protein FLJ10262; FLJ10262		9	
39423_f_at	SPOP	AJ000644	6	Pass	12.50	7.74	11	Pass	TRUE	FALSE	FALSE	5.55	speckle-type POZ protein; SPOP			
39133_at	GCN5L1	A1525379	5	Pass	7.00	2.00	9	Pass	TRUE	FALSE	FALSE	3.11	GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 1; GCN5L1		12q13-q14	
34224_at	KIAA0954	AC004770	6	Pass	4.67	3.33	13	Pass	TRUE	FALSE	FALSE	2.08	retinoid X receptor, alpha; RXRA		9q34.3	
32800_at	RXRA	U66306	6	Pass	56.33	25.13	13	Pass	TRUE	FALSE	FALSE	25.08				
33232_at	CRIP1	A1017574	6	Pass	73.33	19.72	13	Pass	TRUE	FALSE	FALSE	32.69	cysteine-rich protein 1 (intestinal); CRIP1		7q11.23	
33352_at	H2BFQ	X57985	6	Pass	29.67	10.27	13	Pass	TRUE	FALSE	FALSE	13.23	H2B histone family, member Q; H2BFQ		1q21-q23	
38724_at	KIAA0515	AB011087	6	Pass	10.17	1.83	13	Pass	TRUE	FALSE	FALSE	4.54	KIAA0515 protein; KIAA0515			
1505_at	TYMS	D00596	5	Pass	7.00	2.00	8	Pass	TRUE	FALSE	FALSE	3.13	thymidylate synthetase; TYMS		18p11.32	
36984_f_at	HPR	X89214	5	Pass	7.00	2.83	8	Pass	TRUE	FALSE	FALSE	3.13	haptoglobin,haptoglobin-related protein; HP,HPR		16q22.1	
35302_at	TAP	AJ132712	6	Pass	53.50	14.82	13	Pass	TRUE	FALSE	FALSE	23.92	nuclear RNA export factor 1 (Mex67, yeast, homolog); NXF1			
36996_at	OS-9	U41635	6	Pass	66.00	19.85	13	Pass	TRUE	FALSE	FALSE	29.54	amplified in osteosarcoma; OS-9		12q13	
38672_at	PPP1R10	Y13247	6	Pass	22.83	7.78	13	Pass	TRUE	FALSE	FALSE	10.23	protein phosphatase 1, regulatory subunit 10; PPP1R10		6p21.3	
41189_at	TNFRSF12	Y09392	6	Pass	11.50	4.18	13	Pass	TRUE	FALSE	FALSE	5.15	tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein);		1p36.2	
38432_at	ISG15	AA203213	6	Pass	16.50	13.82	10	Pass	TRUE	FALSE	FALSE	7.40	interferon-stimulated protein, 15 kDa; ISG15		1	
38279_at	GNAZ	D90150	6	Pass	11.83	4.62	13	Pass	TRUE	FALSE	FALSE	5.31	guanine nucleotide binding protein (G protein), alpha 2 polypeptide; GNAZ		22q11.22	
38585_at	HBG2	M91036	6	Pass	101.50	94.05	12	Pass	TRUE	FALSE	FALSE	45.58	hemoglobin, gamma A; hemoglobin, gamma G; HBG1,HBG2		11p15.5	
38112_g_at	CSPG2	X15998	6	Pass	69.67	52.00	13	Pass	TRUE	FALSE	FALSE	31.31	chondroitin sulfate proteoglycan 2 (versican); CSPG2		5q14.3	
1274_s_at	CDC34	L22005	6	Pass	10.17	3.25	7	Pass	TRUE	FALSE	FALSE	4.57	cell division cycle 34; CDC34		19p13.3	
1643_g_at	MTA1	U35113	6	Pass	8.00	2.19	10	Pass	TRUE	FALSE	FALSE	3.60	metastasis associated 1; MTA1			
243_g_at	MAP4	M64571	6	Pass	10.00	3.63	10	Pass	TRUE	FALSE	FALSE	4.50	microtubule-associated protein 4; MAP4		3p21	
37346_at	ARF5	M57567	6	Pass	46.67	18.51	12	Pass	TRUE	FALSE	FALSE	21.00	ADP-ribosylation factor 5; ARF5		7q31.3	
37959_at	KIAA0154	D63876	6	Pass	20.00	7.38	13	Pass	TRUE	FALSE	FALSE	9.00	KIAA0154 protein; ADP-ribosylation factor binding protein GGA3; KIAA0154		17	
38663_at	BCKRP1	A1033692	6	Pass	23.50	7.23	12	Pass	TRUE	FALSE	FALSE	10.58	Breakpoint cluster region protein, uerine leiomyoma, 1; barrier to autointegration factor;		14q24.1	

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37844_at	UNK_A120	A1263885	6	Pass	20.67	8.87	13	Pass	TRUE	FALSE	9.31	2.22	class I cytokine receptor; WSX-1	19p13.11	
32607_at	BASP1	AF039656	6	Pass	36.33	21.37	13	Pass	TRUE	FALSE	16.38	2.22	brain acid-soluble protein 1; BASP1	5p14-15	
33396_at	GSTP1	U12472	6	Pass	70.17	32.53	13	Pass	TRUE	FALSE	31.69	2.21	glutathione S-transferase pi; GSTP1	11q13	
39330_s_at	ACTN1	M95178	6	Pass	15.83	5.12	13	Pass	TRUE	FALSE	7.15	2.21	actinin, alpha 1; ACTN1	14q24	
38703_at	UNK_AF0	AF005050	6	Pass	16.17	4.07	13	Pass	TRUE	FALSE	7.31	2.21	aspartyl aminopeptidase; DNPEP		
40723_at	SIT	AJ010059	6	Pass	16.17	4.62	13	Pass	TRUE	FALSE	7.31	2.21	SHIP2 interacting transmembrane adaptor; SIT		
464_s_at	IFI35	U72882	6	Pass	16.17	8.98	13	Pass	TRUE	FALSE	7.31	2.21	interferon-induced protein 35; IFI35	17q21	
32226_at	MAP4	M64571	6	Pass	12.67	4.72	11	Pass	TRUE	FALSE	5.73	2.21	microtubule-associated protein 4; MAP4	3p21	
868_at	TAF2H	U13991	6	Pass	33.33	7.76	13	Pass	TRUE	FALSE	15.08	2.21	TATA box binding protein (TBP)-associated factor, RNA polymerase II, H, 30kD; TAF2H	11p15.3	
38036_at	KIAA0195	D83779	6	Pass	17.33	4.55	13	Pass	TRUE	FALSE	7.85	2.21	KIAA0195 gene product; KIAA0195	17	
37898_r_at	TFF3	A1985964	4	Pass	37.00	14.72	8	Pass	TRUE	FALSE	16.75	2.21	trefoil factor 3 (intestinal); TFF3	21q22.3	
654_at	MX11	L07648	6	Pass	14.17	7.36	12	Pass	TRUE	FALSE	6.42	2.21	MAX-interacting protein 1; MX11	10q24-q25	
33602_at	EDG6	AJ000479	6	Pass	27.17	6.34	13	Pass	TRUE	FALSE	12.31	2.21	endothelial differentiation, G-protein-coupled receptor 6; EDG6	19p13.3	
39308_r_at	UNK_X81	X81637	6	Pass	9.67	2.88	13	Pass	TRUE	FALSE	4.38	2.20	clathrin, light polypeptide (Lcb); CLTB	4q2-q3	
37904_s_at	GNL1	X66436	6	Pass	6.17	1.33	10	Pass	TRUE	FALSE	2.80	2.20	ras homolog gene family, member C; ARHC	1p21-p13	
1395_at	ARHC	L25081	5	Pass	13.00	7.11	11	Pass	TRUE	FALSE	5.91	2.20	glucose phosphate isomerase; GPI	19q13.1	
39122_at	GPI	K03515	6	Pass	33.00	7.87	13	Pass	TRUE	FALSE	15.00	2.20	metallothionein 1B (functional); MT1B	16q13	
609_f_at	MT1B	M13485	4	Pass	27.00	5.72	11	Pass	TRUE	FALSE	12.27	2.20	ribosomal protein L23-like; RPL23L	11p15.5	
34358_at	RPL23L	Z49254	6	Pass	22.67	6.38	13	Pass	TRUE	FALSE	10.31	2.20	glutamate receptor, metabotropic 4; GRM4	6p21.3	
35485_at	GRM4	X80818	5	Pass	53.40	13.24	7	Pass	TRUE	FALSE	24.29	2.20	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase); SMPD1	11p15.4-p15.1	
32574_at	SMPD1	X59960	6	Pass	13.17	4.17	13	Pass	TRUE	FALSE	6.00	2.19			
38259_at	STXBP2	AB002559	6	Pass	12.50	4.32	10	Pass	TRUE	FALSE	5.70	2.19	synuxin binding protein 2; STXBP2	19p13.3-p13.2	
36417_s_at	UNK_AF0	AF035295	6	Pass	15.17	5.23	12	Pass	TRUE	FALSE	6.92	2.19	acyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase); ACAA1	3p23-p22	
35154_at	UNK_W68	W68046	6	Pass	52.33	10.75	8	Pass	TRUE	FALSE	23.88	2.19	hypothetical protein FLJ20386; FLJ20386		
38087_s_at	S100A4	W72186	6	Pass	177.67	62.89	13	Pass	TRUE	FALSE	81.08	2.19	protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog); S100A4	1q21	

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1583_at	TNFRSF11	M32315	6	Pass	92.83	44.60	13	Pass	TRUE	FALSE	FALSE	42.38	2.19	tumor necrosis factor receptor superfamily, member 1B; TNFRSF1B	1p36.3-p36.2	*
214_at	MSX1	M97676	5	Pass	10.40	4.51	8	Pass	TRUE	FALSE	FALSE	4.75	2.19	homeobox homolog 1 (formerly homeobox 7); MSX1	4p16.3-p16.1	*
38789_at	TKT	L12711	6	Pass	97.00	62.34	13	Pass	TRUE	FALSE	FALSE	44.31	2.19	transketolase (Vernicke-Korsakoff syndrome);	3p14.3	
40106_at	E1B-AP5	AJ007509	6	Pass	32.83	11.87	13	Pass	TRUE	FALSE	FALSE	15.00	2.19	E1B-55kDa-associated protein 5; E1B-AP5		
38831_f_at	UNK_AF0	AF053356	6	Pass	67.17	23.27	13	Pass	TRUE	FALSE	FALSE	30.69	2.19	guanine nucleotide binding protein (G protein), beta polypeptide 2; GNB2	7q21.3-q22.1	
1804_at	KLK3	X07730	6	Pass	6.33	1.51	10	Pass	TRUE	FALSE	FALSE	2.90	2.18	kallikrein 3, (prostate specific antigen); KLK3	19q13	
38735_at	KIAA0513	AB011085	6	Pass	24.33	8.55	13	Pass	TRUE	FALSE	FALSE	11.15	2.18	KIAA0513 gene product;		
41443_at	TIC	U63127	6	Pass	25.67	6.02	13	Pass	TRUE	FALSE	FALSE	11.77	2.18	SEC7 homolog; TIC	2q13	
38119_at	GYPC	X12496	6	Pass	56.33	19.66	13	Pass	TRUE	FALSE	FALSE	25.85	2.18	glycophorin C (Gerbich blood group); GYPC	2q14-q21	
39594_f_at	MT1H	R93527	6	Pass	28.67	10.27	13	Pass	TRUE	FALSE	FALSE	13.15	2.18	metallothionein 1H;	16q13	
41421_at	KIAA0909	AB020716	6	Pass	12.17	5.12	12	Pass	TRUE	FALSE	FALSE	5.58	2.18	KIAA0909 protein;		
40712_at	ADAM8	D26579	6	Pass	44.00	15.09	13	Pass	TRUE	FALSE	FALSE	20.23	2.17	a disintegrin and metalloprotease domain 8; ADAM8	10q26.3	
40569_at	ZNF42	M58297	6	Pass	8.33	1.51	12	Pass	TRUE	FALSE	FALSE	3.83	2.17	zinc finger protein 42 (myeloid-specific retinoic acid-responsive); ZNF42	19q13.2-q13.4	
283_at	UQCRC1	L16842	6	Pass	27.17	10.46	12	Pass	TRUE	FALSE	FALSE	12.50	2.17	ubiquinol-cytochrome c reductase core protein 1; UQCRC1	3p21.3	
40100_at	LFP40	U72206	6	Pass	16.00	5.66	11	Pass	TRUE	FALSE	FALSE	7.36	2.17	rho/rac guanine nucleotide exchange factor (GEF) 2; ARHGEF2	1	
1878_g_at	ERCC1	M13194	6	Pass	14.33	4.50	10	Pass	TRUE	FALSE	FALSE	6.60	2.17	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence); ERCC1	19q13.2-q13.3	
37329_at	NDUFV1	AF053070	6	Pass	17.00	6.07	12	Pass	TRUE	FALSE	FALSE	7.83	2.17	NADH dehydrogenase (ubiquinone) flavoprotein 1 (51kD); NDUFV1	11q13	
41177_at	UNK_AW	AW024285	6	Pass	35.33	17.08	13	Pass	TRUE	FALSE	FALSE	16.31	2.17	polymerase (RNA) II (DNA directed)		
41332_at	POLR2E	D38251	6	Pass	19.50	7.34	7	Pass	TRUE	FALSE	FALSE	9.00	2.17	polypeptide E (25kD); POLR2E	19p13.3	
1061_at	IL10RA	U00672	6	Pass	31.00	7.77	13	Pass	TRUE	FALSE	FALSE	14.31	2.17	interleukin 10 receptor, alpha; IL10RA	11q23	*
32529_at	P63	X69910	6	Pass	14.00	8.88	13	Pass	TRUE	FALSE	FALSE	6.46	2.17	transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment; P63	12	
32681_at	SLC9A1	S68616	6	Pass	24.67	6.77	13	Pass	TRUE	FALSE	FALSE	11.38	2.17	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amiloride sensitive); SLC9A1	1p36.1-p35	

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38354_at	CEBPB	X52560	6	Pass	74.00	37.56	13	Pass	TRUE	FALSE	FALSE	34.15	CCAAT/enhancer binding protein (C/EBP), beta; CEBPB	20q13.1	
38397_at	UNK_U09	U09196	6	Pass	19.33	5.24	13	Pass	TRUE	FALSE	FALSE	8.92			
39339_at	KIAA0792	AB018335	6	Pass	20.83	5.19	13	Pass	TRUE	FALSE	FALSE	9.62	KIAA0792 gene product; KIAA0792		
41084_at	UNK_A16	A1659108	6	Pass	12.50	3.62	13	Pass	TRUE	FALSE	FALSE	5.77			
35826_at	SUPT5H	AF040253	6	Pass	16.83	5.08	9	Pass	TRUE	FALSE	FALSE	7.78	suppressor of Ty (S.cerevisiae) 5 homolog; SUPT5H	19q13	
34231_at	UNK_AF0	AF074606	6	Pass	17.50	6.86	11	Pass	TRUE	FALSE	FALSE	8.09	histone acetyltransferase; HBOA	Xq21	
33261_at	HLA-DRB	M16941	6	Pass	146.83	\$4.47	13	Pass	TRUE	FALSE	FALSE	67.92	major histocompatibility complex, class II, DR beta 1; HLA-DRB1	6p21.3	
33213_g_at	RRBP1	AF006751	6	Pass	8.83	5.12	11	Pass	TRUE	FALSE	FALSE	4.09	ribosome binding protein 1 (dog 180kD homolog); RRBPI	20p12	
37148_at	LILRB3	AF025333	6	Pass	44.50	25.98	13	Pass	TRUE	FALSE	FALSE	20.62	leukocyte immunoglobulin like receptor, subfamily B (with TM and ITIM domains), member 3; LILRB3	19q13.4	
35336_at	KIAA0668	AL021707	6	Pass	105.00	25.46	13	Pass	TRUE	FALSE	FALSE	48.77			
505_at	CDC37	U43077	6	Pass	48.50	9.75	13	Pass	TRUE	FALSE	FALSE	22.54	CDC37 (cell division cycle 37, S. cerevisiae, homolog); CDC37	19	
37706_at	GLG1	U28811	6	Pass	14.67	2.50	11	Pass	TRUE	FALSE	FALSE	6.82	Golgi apparatus protein 1; GLG1	16q22-q23	
37650_at	UNK_U41	U41315	6	Pass	43.33	11.57	13	Pass	TRUE	FALSE	FALSE	20.15	inaktin, ring finger protein, 1; MKRN1	7q34	
33360_at	KIAA1004	AB023221	6	Pass	20.33	3.01	13	Pass	TRUE	FALSE	FALSE	9.46	F-box and leucine-rich repeat protein 11; FBXL11		
36933_at	NDRG1	D87953	6	Pass	19.67	6.25	13	Pass	TRUE	FALSE	FALSE	9.15	N-myc downstream regulated; NDRG1	8	
33824_at	KRT8	X74929	6	Pass	24.17	8.61	12	Pass	TRUE	FALSE	FALSE	11.25	CGI-39 protein, keratin 8; KRT8, LOC1079	12q13	
36634_at	BTG2	U72649	6	Pass	38.67	16.39	13	Pass	TRUE	FALSE	FALSE	18.00	BTG family, member 2; BTG2	1q32	
38641_at	UNK_AJ1	AJ133115	6	Pass	15.83	4.75	8	Pass	TRUE	FALSE	FALSE	7.38			
40695_at	IMPDH1	J05272	6	Pass	35.67	14.80	13	Pass	TRUE	FALSE	FALSE	16.62	IMP (inosine monophosphate) dehydrogenase 1; IMPDH1	7q31.3-q32	
39347_at	CLAPS2	X97074	6	Pass	50.67	17.93	13	Pass	TRUE	FALSE	FALSE	23.62	adaptor-related protein complex 2, sigma 1 subunit; AP2S1	19q13.2-q13.3	
39134_at	TOM1	AJ006973	6	Pass	7.50	2.66	10	Pass	TRUE	FALSE	FALSE	3.50	target of myb1 (chicken) homolog; TOM1	22q13.1	
35770_at	ATP6S1	D16469	6	Pass	44.00	20.62	13	Pass	TRUE	FALSE	FALSE	20.54	ATPase, H+-transporting, lysosomal (vacuolar proton pump), subunit 1; ATP6S1	Xq28	
36130_f_at	MT1E	R02331	6	Pass	25.67	6.95	12	Pass	TRUE	FALSE	FALSE	12.00	metallothionein 1E (functional); MT1E	16q13	
506_s_at	STAT5A	U43185	6	Pass	23.83	4.88	13	Pass	TRUE	FALSE	FALSE	11.15	signal transducer and activator of transcription 5A; STAT5A	17q11.2	
32192_g_at	ZNF144	D13969	6	Pass	18.00	4.20	7	Pass	TRUE	FALSE	FALSE	8.43	zinc finger protein 144 (Med-18); ZNF144	17	
32197_at	SLC25A11	AF070548	6	Pass	11.17	4.31	13	Pass	TRUE	FALSE	FALSE	5.23	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11; SLC25A11	17p13.3	
40980_at	UNK_W26	W26477	6	Pass	11.17	2.93	13	Pass	TRUE	FALSE	FALSE	5.23			

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32717_at	NEURL	AF029729	4	Pass	27.75	5.74	8	Pass	TRUE	FALSE	13.00	neutralized (Drosophila)-like; NEURL	10q25.1	
38700_at	CSRP1	M33146	6	Pass	11.83	3.66	11	Pass	TRUE	FALSE	5.55	cysteine and glycine-rich protein 1; CSRP1	1q32	
38718_at	DKFZP586E1519	AL050101	6	Pass	8.00	2.10	12	Pass	TRUE	FALSE	3.75	DKFZP586E1519 protein; DKFZP586E1519		
33390_at	UNK_AA2	AA203487	6	Pass	83.67	49.40	9	Pass	TRUE	FALSE	39.22	glutathione S-transferase pi; GSTP1	11q13	
829_s_at	GSTP1	U21689	6	Pass	51.83	30.04	10	Pass	TRUE	FALSE	24.30	glutathione S-transferase pi; GSTP1	11q13	
39778_at	MGAT1	M55621	6	Pass	39.67	12.47	13	Pass	TRUE	FALSE	18.62	mannosyl (alpha-1,3)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase; MGAT1	5q35	
40153_at	ABCB2	X57522	6	Pass	29.50	8.67	13	Pass	TRUE	FALSE	13.85	ATP-binding cassette, sub-family B (MDR/TAP), member 2; ABCB2	6p21.3	
404_at	IL4R	X52425	6	Pass	29.00	8.29	13	Pass	TRUE	FALSE	13.62	interleukin 4 receptor; IL4R	16p11.2-12.1	
37101_at	DKFZP564A063	AL050008	6	Pass	19.17	5.19	12	Pass	TRUE	FALSE	9.00	DKFZP564A063 protein; DKFZP564A063		
32904_at	PRF1	M28393	6	Pass	86.00	65.71	13	Pass	TRUE	FALSE	40.38	perforin 1 (preforming protein); PRF1	10q22	
33228_g_at	IL10RB	A1984234	6	Pass	55.50	17.95	13	Pass	TRUE	FALSE	26.08	interleukin 10 receptor, beta; IL10RB	21q22.11	
40421_at	PIN1	U49070	6	Pass	8.67	2.58	12	Pass	TRUE	FALSE	4.08	protein (peptidyl-prolyl cis/trans isomerase) NIMA interacting 1; PIN1	19p13	
691_g_at	P4HB	J02783	6	Pass	49.17	17.06	12	Pass	TRUE	FALSE	23.17	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding tumor necrosis factor receptor superfamily, member 1A; TNFRSF1A	17q25	
1563_s_at	TNFRSF1A	M58286	6	Pass	28.17	11.91	11	Pass	TRUE	FALSE	13.27	tubulin, alpha 1 (testis specific); TUBA1	12p13.2	
330_s_at	TUBA1	X06956	6	Pass	39.17	9.47	13	Pass	TRUE	FALSE	18.46	zinc finger protein 266; ZNF266	2q	
41622_r_at	ZNF266	AA868898	6	Pass	6.83	1.83	9	Pass	TRUE	FALSE	3.22	H2A histone family, member O; H2AFO		
286_at	H2AFO	L19779	6	Pass	61.50	25.26	13	Pass	TRUE	FALSE	29.00	peroxisome biogenesis factor 10; PEX10		
41282_s_at	PEX10	AA194159	4	Pass	11.50	3.70	7	Pass	TRUE	FALSE	5.43	interferon induced transmembrane protein 3 (1-8U); IFITM3		
41745_at	IFITM3	X57352	6	Pass	207.17	120.90	13	Pass	TRUE	FALSE	97.85	E74-like factor 4 (cis domain transcription factor); ELF4	Xq26	
31845_at	ELF4	U32645	6	Pass	18.17	7.70	12	Pass	TRUE	FALSE	8.58	CD19 antigen; CD19	16p11.2	
1116_at	CD19	M28170	6	Pass	6.83	1.33	13	Pass	TRUE	FALSE	3.23	linker for activation of T cells; LAT		
40688_at	LAT	AJ223280	6	Pass	27.67	4.37	12	Pass	TRUE	FALSE	13.08	ubiquitin specific protease 11; USP11	Xp21.2-p11.2	
162_at	USP11	U44839	6	Pass	46.17	9.66	13	Pass	TRUE	FALSE	21.85	docking protein 2, 56kD; DOK2		
34906_g_at	UNK_AA9	AA977136	6	Pass	32.50	8.85	13	Pass	TRUE	FALSE	15.38	biflavin reductase B (flavin reductase (NADPH)); BLVRB	19q13.1-q13.2	
31514_at	DOK2	AF034970	6	Pass	25.33	8.80	10	Pass	TRUE	FALSE	12.00	ubiquitin specific protease 4 (proto-oncogene); USP4	3p21.3	
37002_at	BLVRB	D32143	6	Pass	25.00	11.47	13	Pass	TRUE	FALSE	11.85			
1357_at	USP4	U20657	6	Pass	12.33	4.59	13	Pass	TRUE	FALSE	5.85			

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32317_s_at	SULT1A2	U34804	6	Pass	24.50	11.33	13	Pass	TRUE	FALSE	FALSE	11.62	2.11	sulfotransferase family 1A, phenol-preferring, member 2	6p12.1-p11.2	
35774_r_at	NDUFB7	AA527880	6	Pass	24.33	7.55	13	Pass	TRUE	FALSE	FALSE	11.54	2.11	SULT1A2, SULT1A1, NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (18kD, B18); NDUFB7		
40870_g_at	RBM6	AF069517	6	Pass	12.17	3.97	13	Pass	TRUE	FALSE	FALSE	5.77	2.11	RNA binding motif protein 6; RBM6	3p21.3	
39081_at	MT2A	AI547258	6	Pass	11.83	4.31	13	Pass	TRUE	FALSE	FALSE	5.62	2.11	metallothionein 2A; MT2A	16q13	
1375_s_at	TIMP2	M32304	4	Pass	14.75	8.26	9	Pass	TRUE	FALSE	FALSE	7.00	2.11	tissue inhibitor of metalloproteinase 2; TIMP2	17q25	
36615_at	ARP	M83751	4	Pass	19.75	5.50	8	Pass	TRUE	FALSE	FALSE	9.38	2.11	Arginine-rich protein; ARP	3p21.1	
35312_at	MCM2	D21063	6	Pass	17.50	3.62	13	Pass	TRUE	FALSE	FALSE	8.31	2.11	minichromosome maintenance deficient (S. cerevisiae) 2 (uniotin); MCM2	3q21	
37801_at	TJ6	AF112972	6	Pass	9.00	3.58	11	Pass	TRUE	FALSE	FALSE	4.27	2.11	TJ6 protein; TJ6		
38621_at	UNK_A10	AJ012008	6	Pass	10.00	2.45	12	Pass	TRUE	FALSE	FALSE	4.75	2.11	dimethylarginine dimethylaminohydrolase 2; DDAH2	6p21.3	
37939_at	UNK_AL0	AL022318	6	Pass	45.67	11.69	13	Pass	TRUE	FALSE	FALSE	21.69	2.11	small inducible cytokine A5 (RANTES); SCYA5	17q11.2-q12	
1405_i_at	SCYA5	M21121	6	Pass	68.17	25.93	13	Pass	TRUE	FALSE	FALSE	32.38	2.10	tumor necrosis factor receptor superfamily, member 5; TNFRSF5	20q12-q13.2	
35150_at	TNFRSF5	X60592	6	Pass	28.33	7.66	13	Pass	TRUE	FALSE	FALSE	13.46	2.10	hypothetical protein; CGI-57		
34864_at	CGI-57	AF070638	6	Pass	38.17	12.35	13	Pass	TRUE	FALSE	FALSE	18.15	2.10	golgi autoantigen, golgin subfamily a, 3; GOLGA3	12	
34861_at	GOLGA3	D63997	6	Pass	10.83	1.47	13	Pass	TRUE	FALSE	FALSE	5.15	2.10	arginine glutamic acid dipeptide RE repeats; RERE	1p36.1-p36.2	
32253_at	ATN1L	AB007927	6	Pass	31.67	4.97	13	Pass	TRUE	FALSE	FALSE	15.08	2.10	ubiquitin specific protease 15; USP15	12q14	
41264_at	UNK_AL0	AL050172	4	Pass	6.00	2.94	7	Pass	TRUE	FALSE	FALSE	2.86	2.10	C-terminal binding protein 2; CTBP2	21q21.3	
34295_at	USP15	AB011101	6	Pass	6.00	3.16	7	Pass	TRUE	FALSE	FALSE	2.86	2.10	intercellular adhesion molecule 2; ICAM2	17q23-q25	
40780_at	CTBP2	AF016507	6	Pass	15.33	10.46	13	Pass	TRUE	FALSE	FALSE	7.31	2.10	Fe fragment of IgE, high affinity I. receptor for; gamma polypeptide; FCER1G	1q23	
38453_at	ICAM2	X15606	6	Pass	22.50	5.36	13	Pass	TRUE	FALSE	FALSE	12.15	2.10	brain and reproductive organ-expressed (TNFRSF1A modulator); BRE		
36889_at	FCER1G	M33195	6	Pass	56.00	35.60	13	Pass	TRUE	FALSE	FALSE	26.69	2.10	small glutamine-rich tetrapeptide repeat (TPR)-containing; SGT	19p13	
38053_s_at	BRE	AF015767	6	Pass	9.83	3.13	13	Pass	TRUE	FALSE	FALSE	4.69	2.10	tryptophanyl-tRNA synthetase; WARS	14q23-q31	
32816_at	SGT	AL050156	6	Pass	6.67	2.25	11	Pass	TRUE	FALSE	FALSE	3.18	2.10	Trachea Collins-Franceschetti syndrome 1; TCOF1	5q32-q33.1	
36986_at	UNK_AL0	AL031295	6	Pass	117.17	29.18	13	Pass	TRUE	FALSE	FALSE	55.92	2.10			
38121_at	WARS	X59892	6	Pass	34.17	22.83	13	Pass	TRUE	FALSE	FALSE	16.31	2.10			
32877_i_at	UNK_AA5	AA524802	4	Pass	49.50	23.69	11	Pass	TRUE	FALSE	FALSE	23.64	2.09			
40596_at	TCOF1	U76366	6	Pass	22.33	4.55	12	Pass	TRUE	FALSE	FALSE	10.67	2.09			

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39072_at	MXI1	L07648	6	Pass	28.50	13.14	13	Pass	TRUE	FALSE	13.62	2.09	MAX-interacting protein 1; MXI1	10q24-q25	
37033_s_at	GPX1	X13710	6	Pass	279.17	52.77	13	Pass	TRUE	FALSE	133.38	2.09	glutathione peroxidase 1; GPX1	3p21.3	
32195_at	UNK_AL0	AL049450	6	Pass	14.17	5.12	13	Pass	TRUE	FALSE	6.77	2.09			
37390_at	KIAA0224	D86977	6	Pass	13.67	2.94	13	Pass	TRUE	FALSE	6.54	2.09	KIAA0224 gene product; KIAA0224	16	
38449_at	UNK_W28	W28931	6	Pass	15.67	8.94	8	Pass	TRUE	FALSE	7.50	2.09	eukaryotic translation initiation factor 3, subunit 3 (antenna-40kD); EIF3S3		
36187_at	RNH	X13973	6	Pass	39.50	15.10	13	Pass	TRUE	FALSE	18.92	2.09	ribonuclease/angiogenin inhibitor; RNH	11p15.5	
34408_at	RTN2	AF004222	6	Pass	12.00	3.35	8	Pass	TRUE	FALSE	5.75	2.09	retention 2; RTN2		
36798_g_at	SPN	J04168	6	Pass	47.50	14.95	13	Pass	TRUE	FALSE	22.77	2.09	sialophorin (gpL115, leukosialin, CD43); SPN	16p11.2	
38412_at	PPPIR11	U53588	6	Pass	17.00	4.24	13	Pass	TRUE	FALSE	8.15	2.08	protein phosphatase 1, regulatory (inhibitor) subunit 11; PPPIR11	6p21.3	
34033_s_at	LILRA2	AF025531	6	Pass	33.67	18.47	13	Pass	TRUE	FALSE	16.15	2.08	leukocyte immunoglobulin like receptor, subfamily A (with TM domain), member 2; LILRA2	19q13.4	
241_g_at	SRM	M64231	6	Pass	16.67	3.88	12	Pass	TRUE	FALSE	8.00	2.08	spermidine synthase; SRM	1p36-p22	
41316_s_at	SAFB	U72355	6	Pass	20.67	5.05	13	Pass	TRUE	FALSE	9.92	2.08	scaffold attachment factor B; SAFB	19p13	
36591_at	TUBA1	X06956	6	Pass	114.67	24.81	13	Pass	TRUE	FALSE	55.08	2.08	tubulin, alpha 1 (testis specific); TUBA1	2q	
38830_at	ABCF3	U66685	5	Pass	9.20	3.77	7	Pass	TRUE	FALSE	4.43	2.08	ATP-binding cassette, sub-family F (GCN20), member 3, hypothetical protein FLJ11198; ABCF3, FLJ11198	3q25.1-q25.2	
38841_at	GDBR1	AF068195	6	Pass	9.00	4.52	12	Pass	TRUE	FALSE	4.33	2.08	putative glioblastoma cell differentiation-related, putative glioblastoma cell differentiation-related protein; GDBR1, GDBR1	9	
37641_at	MTAP44	D28915	6	Pass	11.50	7.48	13	Pass	TRUE	FALSE	5.54	2.08	interferon-induced, hepatitis C-associated microtubular aggregate protein (44kD); MTAP44	1	
41838_at	UNK_X99	X99270	6	Pass	7.50	2.35	13	Pass	TRUE	FALSE	3.62	2.07	Xq28, 2000bp sequence contig. ORF; HSXQ28ORF		
41614_at	KIAA0708	AB014608	6	Pass	6.83	2.04	10	Pass	TRUE	FALSE	3.30	2.07	KIAA0708 protein; KIAA0708		
448_s_at	MEN1	U93237	6	Pass	6.83	1.83	10	Pass	TRUE	FALSE	3.30	2.07	multiple endocrine neoplasia 1; MEN1	11q13	
32140_at	SORL1	Y08110	6	Pass	81.00	22.91	13	Pass	TRUE	FALSE	39.15	2.07	sortilin-related receptor, L(DLR class) A repeats-containing; SORL1	11q23.2-q24.2	
32592_at	KIAA0323	AB002321	6	Pass	17.17	4.67	13	Pass	TRUE	FALSE	8.31	2.07	KIAA0323 protein; KIAA0323		
36709_at	ITGAX	Y00093	6	Pass	30.83	17.06	13	Pass	TRUE	FALSE	14.92	2.07	integrin, alpha X (antigen CD11C (p150), alpha polypeptide); ITGAX	16p11.2	
41387_r_at	KIAA0346	AB002344	6	Pass	11.50	6.16	7	Pass	TRUE	FALSE	5.57	2.06	KIAA0346 protein; KIAA0346	17p13.1	
41625_at	TRAP240	AB011165	6	Pass	5.83	3.19	12	Pass	TRUE	FALSE	2.83	2.06	thyroid hormone receptor-associated protein, 240 kDa subunit; TRAP240	17	
35254_at	FLN29	AB007447	6	Pass	15.67	4.63	13	Pass	TRUE	FALSE	7.62	2.06	FLN29 gene product; FLN29	12q	

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38780_at	AKR1A1	J04794	6	Pass	28.00	8.65	13	Pass	TRUE	FALSE	FALSE	13.62	aldo-keto reductase family 1, member A1 (aldehyde reductase); AKR1A1	1p33-p32	
40890_at	MTX1	U46920	6	Pass	27.83	7.55	13	Pass	TRUE	FALSE	FALSE	13.54	metaxin 1; MTX1	1q21	
39412_at	ZNF173	U09825	6	Pass	12.33	5.57	9	Pass	TRUE	FALSE	FALSE	6.00	zinc finger protein 173; ZNF173	6p21.3	
33215_g_at	RPMS12	Y11681	6	Pass	33.67	6.53	13	Pass	TRUE	FALSE	FALSE	16.38	ribosomal protein, mitochondrial, S12; RPMS12	19q13.1	
34310_at	APRT	Y00486	5	Pass	25.40	6.27	11	Pass	TRUE	FALSE	FALSE	12.36	adenine phosphoribosyltransferase; APRT	16q24	
33409_at	FKBP2	AA158243	6	Pass	15.00	4.65	13	Pass	TRUE	FALSE	FALSE	7.31	FK506-binding protein 2 (13kD); FKBP2	11q13.1-q13.3	
33748_at	KIAA0223	D86976	6	Pass	53.50	13.14	13	Pass	TRUE	FALSE	FALSE	26.08	minor histocompatibility antigen HA-1; KIAA0223	19p13.3	
33323_r_at	SFN	X57348	6	Pass	11.50	4.72	13	Pass	TRUE	FALSE	FALSE	5.62	stratifin; SFN	1p	
32228_at	ADTAB	AB020706	5	Pass	19.60	6.77	7	Pass	TRUE	FALSE	FALSE	9.57	adaptor-related protein 11 complex 2, alpha 2 subunit; AP2A2	11	
32236_at	UBE2G2	AF032456	6	Pass	25.17	11.18	13	Pass	TRUE	FALSE	FALSE	12.31	ubiquitin-conjugating enzyme E2G 2 (homologous to yeast UBC7); UBE2G2	21q22.3	
32629_f_at	BTN3A1	U90552	6	Pass	111.33	28.98	13	Pass	TRUE	FALSE	FALSE	54.46	butyrophilin, subfamily 3, member A1; BTN3A1	6p22.1	
35769_at	GPR56	AJ011001	6	Pass	23.17	9.30	12	Pass	TRUE	FALSE	FALSE	11.33	G protein-coupled receptor 56; GPR56	16q13	
39541_at	UNK_W52	W52003	4	Pass	12.00	4.08	8	Pass	TRUE	FALSE	FALSE	5.88	microsperic protein 1; MCRS1	12	
33898_at	MCRS1	AF015308	6	Pass	16.33	5.28	8	Pass	TRUE	FALSE	FALSE	8.00	microsperic protein 1; MCRS1	12	
36155_at	KIAA0275	D87465	6	Pass	67.83	11.11	13	Pass	TRUE	FALSE	FALSE	33.23	KIAA0275 gene product; KIAA0275	10	
709_at	UNK_J003	J00314	6	Pass	16.50	3.62	11	Pass	TRUE	FALSE	FALSE	8.09	tubulin, beta polypeptide; TUBB	6p21.3	
37147_at	SCGF	AF020044	6	Pass	18.33	5.85	12	Pass	TRUE	FALSE	FALSE	9.00	stem cell growth factor; lymphocyte secreted C-type lectin; SCGF	19q13.3	
39865_at	UNK_A181	A1890903	6	Pass	9.67	2.66	12	Pass	TRUE	FALSE	FALSE	4.75	RNA binding motif protein 3p21.3; RBM6	3p21.3	
40869_at	RBM6	AF069517	6	Pass	9.67	2.73	12	Pass	TRUE	FALSE	FALSE	4.75	RNA binding motif protein 3p21.3; RBM6	3p21.3	
35282_r_at	CD81	M33680	6	Pass	77.33	22.92	13	Pass	TRUE	FALSE	FALSE	38.00	CD81 antigen (target of antiproliferative antibody 1); CD81	11p15	
39141_at	ABCF1	AF027302	6	Pass	12.83	4.17	13	Pass	TRUE	FALSE	FALSE	6.31	ATP-binding cassette, subfamily F (GCN20), member 1; ABCF1	6p21.33	
715_s_at	GGT1	D87002	6	Pass	7.67	2.07	13	Pass	TRUE	FALSE	FALSE	3.77	gamma-glutamyltransferase 1; gamma-glutamyltransferase 2; signal transducer and activator of transcription 1; 91kD; STAT1	22q11.1-q11.2,22q11.23	
33338_at	STAT1	M97936	6	Pass	20.00	9.80	12	Pass	TRUE	FALSE	FALSE	9.83	signal transducer and activator of transcription 1; 91kD; STAT1	2q32.2	
38257_at	NDUFS8	AF038406	6	Pass	10.17	5.56	10	Pass	TRUE	FALSE	FALSE	5.00	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase);	11q13	
32553_at	MAZ	M94046	6	Pass	96.33	20.40	13	Pass	TRUE	FALSE	FALSE	47.38	MYC-associated zinc finger protein (purine-binding transcription small inducible cytokine AS (RANTES); SCYA5	16p11.2	
1404_r_at	SCYA5	M21121	6	Pass	10.50	3.94	12	Pass	TRUE	FALSE	FALSE	5.17	small inducible cytokine AS (RANTES); SCYA5	17q11.2-q12	
37256_at	UNK_A182	A1829890	6	Pass	10.83	2.86	12	Pass	TRUE	FALSE	FALSE	5.33			

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Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (Normal)	Fold Change RA / Normal	Name	Chromosome	Kinase or Phosphatase
40494_at	DEDD	AF043733	6	Pass	21.67	9.05	12	Pass	TRUE	FALSE	FALSE	10.67	2.03	death effector domain-containing; DEDD		
38864_at	UNK_W26	W26851	6	Pass	13.00	2.00	10	Pass	TRUE	FALSE	FALSE	6.40	2.03			
41267_at	KIAA1049	AB028972	6	Pass	22.33	6.95	13	Pass	TRUE	FALSE	FALSE	11.00	2.03	KIAA1049 protein;	16	
32080_at	TETRA	L11669	6	Pass	42.17	12.22	13	Pass	TRUE	FALSE	FALSE	20.77	2.03	KIAA1049 tetraacycline transporter-like protein; TETRA	4p16.3	*
35944_at	UNK_AL0	AL031228	5	Pass	14.20	5.54	7	Pass	TRUE	FALSE	FALSE	7.00	2.03	Cluster Incl AL031228; Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BING5 gene, exons 11 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RING5), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG	6p21.3	*
33388_at	UNK_AL0	AL080223	6	Pass	22.00	5.40	13	Pass	TRUE	FALSE	FALSE	10.85	2.03			
40787_at	UNK_U90	U90911	6	Pass	12.17	3.66	13	Pass	TRUE	FALSE	FALSE	6.00	2.03	matrix metalloproteinase-like 1; MMP1	16p13.3	
35911_at	MMPL1	AJ003147	6	Pass	24.50	8.14	12	Pass	TRUE	FALSE	FALSE	12.08	2.03	CD63 antigen (melanoma antigen); CD63	12q12-q13	
37003_at	CD63	X62654	6	Pass	29.00	14.71	13	Pass	TRUE	FALSE	FALSE	14.31	2.03	Dynamin (dynactin complex 50 kD subunit);	12	
38475_at	DCTN-50	U50733	6	Pass	14.50	5.54	13	Pass	TRUE	FALSE	FALSE	7.15	2.03	DCTN-50	16q13	
870_f_at	MT3	M93311	6	Pass	31.50	13.44	11	Pass	TRUE	FALSE	FALSE	15.55	2.03	metallothionein 3 (growth inhibitory factor (neurotrophic)); MT3	6p21.3	
34178_at	UNK_A188	A1884738	6	Pass	7.17	1.60	13	Pass	TRUE	FALSE	FALSE	3.54	2.03	zinc finger protein 297; ZNF297	1p32.3	
36167_at	ATP6F	D89052	6	Pass	64.50	29.51	13	Pass	TRUE	FALSE	FALSE	31.85	2.03	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD; STX4A		
37911_at	STX4A	U07158	6	Pass	13.33	3.88	12	Pass	TRUE	FALSE	FALSE	6.58	2.03	U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2; U2AF1RS2	Xp22.1	
38523_c_at	U2AF1RS2	D49677	6	Pass	13.67	2.58	12	Pass	TRUE	FALSE	FALSE	6.75	2.02	centromere protein B (80kD); CENPB	20p13	
37931_at	CENPB	X05299	6	Pass	10.67	2.42	11	Pass	TRUE	FALSE	FALSE	5.27	2.02	arachidonate 12-lipoxygenase; ALOX12	17p13.1	
35124_at	ALOX12	M62982	6	Pass	14.00	4.69	13	Pass	TRUE	FALSE	FALSE	6.92	2.02			

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32523_at	CLTB	M20470	6	Pass	5.17	1.83	9	Pass	TRUE	FALSE	FALSE	2.56	clathrin, light polypeptide (Lcb); CLTB	4q2-q3	
37442_at	UNK_AL0	AL050378	6	Pass	18.00	6.32	13	Pass	TRUE	FALSE	FALSE	8.92	oxoglutarate dehydrogenase	7p14-p13	
40470_at	OGDH	D10523	5	Pass	14.40	3.85	7	Pass	TRUE	FALSE	FALSE	7.14	Lysosomal-associated multispanning membrane protein-5; LAPTM5	1p34	
37759_at	LAPTM5	U51240	6	Pass	229.50	56.06	13	Pass	TRUE	FALSE	FALSE	113.85	Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro); SSA1	11p15.5	
37126_at	SSA1	M62800	5	Pass	15.00	5.83	9	Pass	TRUE	FALSE	FALSE	7.44	heat shock protein 75; TRAP1	16	
34260_at	KIAA0683	AB014583	5	Pass	6.80	2.49	8	Pass	TRUE	FALSE	FALSE	3.38	inositol 1,4-5-bisphosphate 3-kinase B; transforming growth factor, beta 1; TGFB1	16	
1468_at	TRAP1	U12595	6	Pass	11.00	2.10	13	Pass	TRUE	FALSE	FALSE	5.46	ring finger protein 1; RING1	1q41-q43	kinase
37272_at	ITPKB	X57206	6	Pass	28.50	6.38	13	Pass	TRUE	FALSE	FALSE	14.15	v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (n65)); RELA	11q13	
1830_s_at	TGFB1	M38449	6	Pass	30.67	6.80	13	Pass	TRUE	FALSE	FALSE	15.23	FOS-like antigen-1; FOSL1	11q13	
35685_at	RING1	Z14000	6	Pass	15.33	3.93	13	Pass	TRUE	FALSE	FALSE	7.62	aquaporin 9; AQP9	7p14-p12	
1295_at	RELA	L19067	6	Pass	39.17	15.38	13	Pass	TRUE	FALSE	FALSE	19.46	acyloxycyl hydrolase (neutrophil); AOA1		
32271_at	FOSL1	X16707	4	Pass	9.25	2.75	10	Pass	TRUE	FALSE	FALSE	4.60	prostatic binding protein; PBP		
34435_at	AQP9	AB008775	6	Pass	7.83	5.19	10	Pass	TRUE	FALSE	FALSE	3.90	MYC promoter-binding protein 1, enolase 1, (alpha); ENO1; MPB1	1p36.3-p36.2, 1p36.1	
37647_at	AOAH	M62840	6	Pass	25.00	14.34	13	Pass	TRUE	FALSE	FALSE	12.46	capping protein (actin filament) muscle Z-line, beta; CAPZB		
32611_at	PBP	X75252	6	Pass	14.50	5.09	13	Pass	TRUE	FALSE	FALSE	7.23	MAP-kinase activating death domain; MADD	11p11.2	
2035_s_at	MPB1	M55914	6	Pass	125.67	55.44	13	Pass	TRUE	FALSE	FALSE	62.69	KIAA0140 gene product; KIAA0140		
37012_at	CAPZB	U03271	6	Pass	65.83	19.11	13	Pass	TRUE	FALSE	FALSE	32.85	DKFZP586B0519 protein; DKFZP586B0519		
34830_at	UNK_W25	W25986	6	Pass	36.83	7.31	13	Pass	TRUE	FALSE	FALSE	18.38	Src-like-adaptor SLA	8q24	
38398_at	MADD	AB002356	6	Pass	16.33	6.09	13	Pass	TRUE	FALSE	FALSE	8.15	tetratricopeptide repeat domain 2; TTC2	17q11.2	
40143_at	KIAA0140	D50930	6	Pass	18.33	7.23	13	Pass	TRUE	FALSE	FALSE	9.15	papillary renal cell carcinoma (translocation-associated); PRCC	1q21.1	
35205_at	DKFZP586	AL050280	6	Pass	32.50	9.40	13	Pass	TRUE	FALSE	FALSE	16.23	solute carrier family 1 (neutral amino acid transporter), member 5; SLC1A5	19q13.3	
1427_g_at	SLA	D89077	6	Pass	22.33	10.86	13	Pass	TRUE	FALSE	FALSE	11.15	SH2-B homolog; DKFZP547G1110		
41800_s_at	TTC2	U46571	6	Pass	22.33	5.65	13	Pass	TRUE	FALSE	FALSE	11.15			
39149_at	PRCC	X99720	6	Pass	10.00	2.00	7	Pass	TRUE	FALSE	FALSE	5.00			
41778_at	SLC1A5	U53347	5	Pass	8.00	3.61	8	Pass	TRUE	FALSE	FALSE	4.00			
40149_at	DKFZP547	AL049924	6	Pass	7.00	0.63	8	Pass	TRUE	FALSE	FALSE	3.50			

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453_at	SMARCC2	U66616	6	Pass	5.00	2.00	8	Pass	TRUE	FALSE	FALSE	2.50	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2;	12q13-q14	
40840_at	PPIF	M80254	6	Pass	8.67	2.66	9	Pass	TRUE	FALSE	FALSE	4.33	SMARCC2 peptidylprolyl isomerase F (cyclophilin F); PPIF	10q22-q23	
1014_at	POLG	U60325	6	Pass	10.00	3.41	12	Pass	TRUE	FALSE	FALSE	5.00	polymyrase (DNA directed), gamma; POLG	15q25	
1243_at	DDB2	U18300	6	Pass	11.00	1.79	12	Pass	TRUE	FALSE	FALSE	5.50	damage-specific DNA binding protein 2 (48kD); DDB2	11p12-p11	
1487_at	ESRRA	L38487	6	Pass	12.00	5.18	12	Pass	TRUE	FALSE	FALSE	6.00	estrogen-related receptor alpha; ESRRA	11q12	
197_at	NME3	U29656	6	Pass	10.50	2.88	12	Pass	TRUE	FALSE	FALSE	5.25	non-metastatic cells 3, protein expressed in; NME3	16q13	
32533_s_at	VAMP5	AF054825	6	Pass	9.50	4.23	12	Pass	TRUE	FALSE	FALSE	4.75	vesicle-associated membrane protein 5 (nvabrevin); VAMP5		
34871_at	UNK W30	W30677	6	Pass	18.67	6.83	12	Pass	TRUE	FALSE	FALSE	9.33			
36815_at	UNK AF0	AF038185	6	Pass	16.00	3.41	12	Pass	TRUE	FALSE	FALSE	8.00			
40282_s_at	IDF	M84526	6	Pass	38.00	25.78	13	Pass	TRUE	FALSE	FALSE	19.00	D component of complement (adipsin); DF	19	
36645_at	RELA	L19067	6	Pass	33.67	12.82	13	Pass	TRUE	FALSE	FALSE	16.85	v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (n65)); RELA	11q13	
41471_at	SI00A9	W72424	6	Pass	313.50	166.70	13	Pass	TRUE	FALSE	FALSE	157.00	SI00 calcium-binding protein A9 (calgranulin B); SI00A9	1q21	
33227_at	IL10RB	A1984234	6	Pass	15.33	6.22	13	Pass	TRUE	FALSE	FALSE	7.69	interleukin 10 receptor, beta; IL10RB	21q22.11	
38308_s_at	KIAA0607	AB011179	6	Pass	30.50	9.31	13	Pass	TRUE	FALSE	FALSE	15.31	neurochondrin; KIAA0607	1	
36145_at	SIAHBP1	U51586	6	Pass	22.50	6.77	13	Pass	TRUE	FALSE	FALSE	11.31	siah binding protein 1; FBP interacting repressor; pyrimidine tract binding splicing factor; Ro ribonucleoprotein-binding protein 1; SIAHBP1	8q24.2-qtel	
40469_at	MCM3AP	AB011144	6	Pass	22.50	6.66	13	Pass	TRUE	FALSE	FALSE	11.31	minichromosome maintenance deficient (S. cerevisiae) 3-associated protein; MCM3AP	21q22.3	
1506_at	IL2RG	D11086	6	Pass	26.33	8.02	12	Pass	TRUE	FALSE	FALSE	13.25	interleukin 2 receptor, gamma (severe combined immunodeficiency);	Xq13.1	
33781_s_at	UBE2M	AF075599	6	Pass	6.50	2.43	11	Pass	TRUE	FALSE	FALSE	3.27	ubiquitin-conjugating enzyme E2M (homologous to yeast UBC12); UBE2M		
40501_s_at	MYBPC1	X73114	5	Pass	14.20	4.44	13	Pass	TRUE	FALSE	FALSE	7.15	myosin-binding protein C, slow-type; MYBPC1	12	
35267_s_at	BC10	AL049288	6	Pass	14.33	4.93	13	Pass	TRUE	FALSE	FALSE	7.23	bladder cancer associated protein; BLCAP	20	
36959_at	UBE2V1	U49278	6	Pass	25.00	9.98	13	Pass	TRUE	FALSE	FALSE	12.62	hypothetical protein DKFZp547H084.ubiquitin-conjugating enzyme E2 variant 1; DKFZp547H084.UBE2V1	20q13.2	
32967_at	TOSO	AF057557	6	Pass	23.00	7.46	13	Pass	TRUE	FALSE	FALSE	11.62	regulator of Fas-induced apoptosis; TOSO		

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38338_at	RRAS	AI201108	6	Pass	15.83	5.53	12	Pass	TRUE	FALSE	8.00	1.98	related RAS viral (r-ras) oncogene homolog; RRAS	19q13.3-qter	
34892_at	TNFRSF10	AF016266	6	Pass	15.83	5.49	13	Pass	TRUE	FALSE	8.00	1.98	tumor necrosis factor receptor superfamily, member 10b; TNFRSF10B	8p22-p21	
38181_at	MMP11	X57766	6	Pass	11.33	4.41	11	Pass	TRUE	FALSE	5.73	1.98	matrix metalloproteinase 11 (stromelysin 3);	22q11.23	
31826_at	KIAA0674	AB014574	6	Pass	28.00	9.40	13	Pass	TRUE	FALSE	14.15	1.98	KIAA0674 protein;	9	
34347_at	DKFZP564	AL049955	6	Pass	22.67	5.24	13	Pass	TRUE	FALSE	11.46	1.98	DKFZP564J0123 protein;	3p21.2-24.2	
40076_at	TPD52L2	AF004430	6	Pass	22.67	11.27	13	Pass	TRUE	FALSE	11.46	1.98	tumor protein D52-like 2; TPD52L2	20q13.2-q13.3	
37967_at	D6S49E	AF000424	6	Pass	100.17	51.60	13	Pass	TRUE	FALSE	50.69	1.98	DNA segment on chromosome 6 (unique) 49 expressed sequence; D6S49E Homo sapiens LST1 mRNA	6p21.3	
37487_at	KIAA1093	AB029016	6	Pass	10.33	3.88	13	Pass	TRUE	FALSE	5.23	1.98	KIAA1093 protein;	22	
41522_at	MFNG	Z93096	6	Pass	10.33	3.72	13	Pass	TRUE	FALSE	5.23	1.98	manic fringe (Drosophila) homolog; MFNG	22q12	
36637_at	ANXA11	L19605	6	Pass	25.83	7.41	13	Pass	TRUE	FALSE	13.08	1.98	annexin A11; ANXA11	10q22-q23	
553_at	ARHGAP1	U02570	6	Pass	43.00	15.65	13	Pass	TRUE	FALSE	21.77	1.98	Rho GTPase activating protein 1; ARHGAP1		
32201_at	SSNA1	Z96932	4	Pass	19.50	7.19	8	Pass	TRUE	FALSE	9.88	1.97	Sjogren's syndrome nuclear autoantigen 1;		
39180_at	FUS	S62140	6	Pass	47.83	13.29	13	Pass	TRUE	FALSE	24.23	1.97	fusion, derived from t(12;16) malignant liposarcoma; FUS	16p11.2	
1062_at	IL10RA	U00672	6	Pass	47.67	15.71	13	Pass	TRUE	FALSE	24.15	1.97	interleukin 10 receptor, alpha, IL10RA	11q23	
41375_at	UNK_AJ24	AJ245416	6	Pass	15.17	5.88	13	Pass	TRUE	FALSE	7.69	1.97	Homo sapiens LST1 mRNA		
36199_at	DAP	X76105	6	Pass	21.67	3.88	12	Pass	TRUE	FALSE	11.00	1.97	death-associated protein; DAP	5p15.2	
37345_at	CALU	AF013759	5	Pass	6.40	1.14	12	Pass	TRUE	FALSE	3.25	1.97	calumenin; CALU	7q32	
38657_at	CLTA	M20471	6	Pass	43.17	19.93	13	Pass	TRUE	FALSE	21.92	1.97	clathrin, light polypeptide (Lca); CLTA	12q23-q24	
32490_at	CEACAM4	AC005955	5	Pass	9.00	2.92	7	Pass	TRUE	FALSE	4.57	1.97	carcinoembryonic antigen-related cell adhesion molecule 4; CEACAM4	19q13.2	
37739_at	SSRP1	M86737	6	Pass	16.50	4.55	13	Pass	TRUE	FALSE	8.38	1.97	structure specific recognition protein 1; SSRP1	11q12	
32806_at	BZRP	M36035	6	Pass	248.17	116.68	13	Pass	TRUE	FALSE	126.15	1.97	benzodiazepine receptor (peripheral); BZRP	22q13.31	
31891_at	CHI3L2	U58515	6	Pass	6.33	1.51	9	Pass	TRUE	FALSE	3.22	1.97	chitinase 3-like 2; CHI3L2	1p13.3	
31801_at	UNK_A180	A1808712	6	Pass	13.00	6.26	13	Pass	TRUE	FALSE	6.62	1.97	nardilysin (N-arginine dipeptide convertase); NRDL	1p32.2-p32.1	
34787_at	NRD1	X93209	6	Pass	32.17	9.64	13	Pass	TRUE	FALSE	16.38	1.96	dibasic convertase; NRD1	17q25	
36666_at	P4HB	M22806	6	Pass	77.17	21.94	13	Pass	TRUE	FALSE	39.31	1.96	oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding		
39738_at	APOL	Z82215	6	Pass	152.17	26.57	13	Pass	TRUE	FALSE	77.62	1.96	small nuclear ribonucleoprotein polypeptide A; SNRPA		
40842_at	SNRPA	M60784	6	Pass	36.17	8.80	13	Pass	TRUE	FALSE	18.46	1.96		19q13.1	

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39551_at	UNK_N98	N98667	6	Pass	25.00	9.57	13	Pass	TRUE	FALSE	FALSE	12.77	1.96	hypothetical protein: LOC51317		
35017_f_at	UNK_M80	M80469	6	Pass	129.67	39.72	13	Pass	TRUE	FALSE	FALSE	66.23	1.96	Cluster Incl M80469: Human MHC class I HLA- J gene, exons 1-8 and complete cds.		
894_g_at	E2-EPF	M91670	6	Pass	13.50	4.85	10	Pass	TRUE	FALSE	FALSE	6.90	1.96	ubiquitin carrier protein: E2-EPF	17	
590_at	ICAM2	M32334	6	Pass	26.33	4.72	13	Pass	TRUE	FALSE	FALSE	13.46	1.96	intercellular adhesion molecule 2; ICAM2	17q23- q25	
34346_at	PRKAG1	U42412	6	Pass	16.83	6.01	13	Pass	TRUE	FALSE	FALSE	8.62	1.95	protein kinase, AMP- activated, gamma 1 non- catalytic subunit;	12q12- q14	
39500_s_at	UNK_AL0	AL049299	5	Pass	8.40	2.70	10	Pass	TRUE	FALSE	FALSE	4.30	1.95	NADH dehydrogenase (ubiquinone) Fe-S protein		
34863_at	NDUFS6	A1360249	5	Pass	9.60	4.34	12	Pass	TRUE	FALSE	FALSE	4.92	1.95	6 (13kD) (NADH- coenzyme Q reductase); major histocompatibility complex, class II, DM alpha; HLA-DMA		
37344_at	HLA-DMA	X62744	6	Pass	51.50	18.12	13	Pass	TRUE	FALSE	FALSE	26.38	1.95	actin related protein 2/3 complex, subunit 4 (20 kD); ARPC4	6p21.3	
34692_r_at	ARPC4	AF006087	6	Pass	22.67	7.84	13	Pass	TRUE	FALSE	FALSE	11.62	1.95	ATX1 (antioxidant protein 5q22 1, yeast) homolog 1; ATOX1		
41776_at	ATOX1	U70660	6	Pass	13.33	4.50	12	Pass	TRUE	FALSE	FALSE	6.83	1.95	synaptophysin 2; SYNGR2	17qter	
34885_at	SYNGR2	A1002308	6	Pass	75.17	17.66	13	Pass	TRUE	FALSE	FALSE	38.54	1.95	ubiquitin carrier protein: E2-EPF	17	
803_at	E2-EPF	M91670	5	Pass	7.80	1.79	9	Pass	TRUE	FALSE	FALSE	4.00	1.95	MD-2 protein; MD-2	8	
33936_at	MD-2	AB018549	6	Pass	13.50	7.89	13	Pass	TRUE	FALSE	FALSE	6.92	1.95	dolichyl-phosphate mannosyltransferase		
38725_s_at	DPM2	N36295	6	Pass	10.50	3.56	13	Pass	TRUE	FALSE	FALSE	5.38	1.95	polypeptide 2, regulatory subunit; DPM2		
40928_at	DKFZP564	W26496	6	Pass	10.50	8.41	13	Pass	TRUE	FALSE	FALSE	5.38	1.95	small inducible cytokine A3 (homologous to mouse Mip-1a); SCYA3	17q11- q21	
39811_at	UNK_AA4	AA402538	6	Pass	26.83	8.45	13	Pass	TRUE	FALSE	FALSE	13.77	1.95	polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I); PTB	14q23- q24.1	
36103_at	SCYA3	D90144	6	Pass	6.33	2.80	12	Pass	TRUE	FALSE	FALSE	3.25	1.95	Human BRCA2 region, mRNA sequence CG006.		
40593_at	PTB	X66975	6	Pass	64.00	23.03	13	Pass	TRUE	FALSE	FALSE	32.85	1.95	granzyme M (lymphocyte met-ase 1); GZMM	19p13.3	
1532_g_at	UNK_U50	U50535	6	Pass	16.33	3.44	13	Pass	TRUE	FALSE	FALSE	8.38	1.95	chemokine (C-C motif) receptor 7; CCR7	17q12- q21.2	
32264_at	UNK_L23	L23134	5	Pass	29.60	14.67	10	Pass	TRUE	FALSE	FALSE	15.20	1.95	US snRNP-specific protein (220 kD), ortholog of S.	17p13.3	
1097_s_at	CCR7	L31584	6	Pass	44.33	27.45	13	Pass	TRUE	FALSE	FALSE	22.77	1.95	cerevisiae Prp8; PRP8		
33753_at	PRP8	AB007510	6	Pass	56.00	9.06	13	Pass	TRUE	FALSE	FALSE	28.77	1.95	KIAA0397 gene product; KIAA0397		
36129_at	UNK_AB0	AB007857	6	Pass	25.00	4.69	13	Pass	TRUE	FALSE	FALSE	12.85	1.95	antizyme inhibitor,protease, serine, 15; LOC51582,PRSS15		
33367_s_at	LOC51582	D88674	6	Pass	4.33	2.34	10	Pass	TRUE	FALSE	FALSE	8.50	-1.96	#N/A	19p13.2.8	
AFFX-M2783	M2783	M27830	6	Pass	9.17	6.01	13	Pass	TRUE	FALSE	FALSE	18.46	-2.01	#N/A	#N/A	

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Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Fold Change (Normal) RA / Normal	Name	Chromosome	Kinase or Phosphatase
34642_at	YWHAZ	U28964	6	Pass	15.17	10.83	13	Pass	TRUE	FALSE	FALSE	30.62	tyrosine 3-monooxygenase/tytiophan 5-monooxygenase activation protein, zeta polypeptide, YWHAZ	2p25.2-p25.1	

qualifier	name	sum of abs dec	4 of 6 present	Avg Freq RA	Std Dev RA	sum of 7 of 13 abs present dec	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Avg Freq (Normal)	Fold Change RA/Normal	Name	Chromos ome	
1642_at	MTA1	U35113	4	Pass	4.75	1.26	0 Fail	FALSE	TRUE	FALSE	#DIV/0!	metastasis associated 1; MTA1		
37963_at	ARSA	X52151	4	Pass	3.50	1.73	0 Fail	FALSE	TRUE	FALSE	#DIV/0!	arylsulfatase A; ARSA	22q13.33	
38350_at	TUBA2	AF005392	4	Pass	10.25	1.26	0 Fail	FALSE	TRUE	FALSE	#DIV/0!	tubulin, alpha 2; TUBA2	13q11	
40800_at	UNK_A155	A1590869	4	Pass	6.75	1.71	0 Fail	FALSE	TRUE	FALSE	#DIV/0!	hypothetical protein similar to mouse HNI (Hematological and Neurological expressed sequence 1); HN1L	16	
38021_at	PLEC1	U53204	6	Pass	22.17	10.91	0 Fail	FALSE	TRUE	FALSE	#DIV/0!	plectin 1, intermediate filament binding protein, 500kD; PLEC1	8q24	
1257_at	QSCN6	L42379	4	Pass	19.00	18.57	1 Fail	FALSE	TRUE	FALSE	3.00	6.33	guanine Q6; QSCN6	1q24
39128_at	PPP2R4	X73478	4	Pass	7.25	5.68	2 Fail	FALSE	TRUE	FALSE	1.50	4.83	protein phosphatase 2A, regulatory subunit B' (PR 53); PPP2R4	9q34
545_at	NFKB2	S76638	4	Pass	4.50	1.29	1 Fail	FALSE	TRUE	FALSE	1.00	4.50	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100); NFKB2	10q24
37769_at	EDG4	AF011466	6	Pass	20.50	4.32	1 Fail	FALSE	TRUE	FALSE	5.00	4.10	endothelial differentiation, lysophosphatidic acid G- protein-coupled receptor, 4; EDG4	19p12
2049_at	JUNB	M29039	5	Pass	10.80	7.19	6 Fail	FALSE	TRUE	FALSE	2.67	4.05	jun B proto-oncogene; JUNB	19p13.2
39145_at	MYRL2	J02854	6	Pass	19.33	9.24	1 Fail	FALSE	TRUE	FALSE	5.00	3.87	myosin regulatory light chain 2, smooth muscle isoform; MYRL2	
32151_at	RANGAP1	X82260	4	Pass	12.25	2.63	2 Fail	FALSE	TRUE	FALSE	3.50	3.50	Ran GTPase activating protein 1; RANGAP1	22q13.2- q13.31
34367_at	PHGDH	AF006043	6	Pass	5.83	3.43	3 Fail	FALSE	TRUE	FALSE	1.67	3.50	3-phosphoglycerate dehydrogenase; PHGDH	1p11.1- 13.1
31596_at	UNK_L021	L02326	6	Pass	46.50	17.20	4 Fail	FALSE	TRUE	FALSE	13.50	3.44	immunoglobulin lambda- like polypeptide 2; IGLL2	22q11.23
34105_at	UNK_A114	A1147237	4	Pass	53.75	31.42	6 Fail	FALSE	TRUE	FALSE	15.67	3.43	endothelial cell growth factor 1 (platelet-derived); ECGF1	
1665_at	ECGF1	M63193	4	Pass	77.75	68.10	3 Fail	FALSE	TRUE	FALSE	23.33	3.33	endothelial cell growth factor 1 (platelet-derived); ECGF1	22q13.33
1855_at	FGF3	X14445	4	Pass	6.50	2.65	3 Fail	FALSE	TRUE	FALSE	2.00	3.25	fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int 2) oncogene homolog); FGF3	11q13
36151_at	HU-K4	U60644	5	Pass	13.00	4.47	5 Fail	FALSE	TRUE	FALSE	4.00	3.25	similar to vaccinia virus HindIII K4L ORF; HU-K4	
32133_at	PIP5K1C	AB011161	6	Pass	14.67	5.99	5 Fail	FALSE	TRUE	FALSE	4.60	3.19	phosphatidylinositol-4- phosphate 5-kinase, type I, gamma; PIP5K1C	19

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41659_at	SUPT6H	U46691	4	Pass	4.50	2.38	2	Fail	FALSE	TRUE	FALSE	1.50	3.00	suppressor of Ty (S.cerevisiae) homolog; SUPT6H	17q11.2	
36158_at	DCTN1	AF086947	5	Pass	7.80	1.92	5	Fail	FALSE	TRUE	FALSE	2.60	3.00	dynactin 1 (p150, Glued (Drosophila) homolog); DCTN1	2p13	
35936_g_at	CPT1B	Y08683	5	Pass	8.00	2.35	4	Fail	FALSE	TRUE	FALSE	2.75	2.91	palmitoyltransferase I, muscle; CPT1B	22q13.33	
41458_at	KIAA0467	AB007936	4	Pass	14.50	5.20	1	Fail	FALSE	TRUE	FALSE	5.00	2.90	KIAA0467 protein; KIAA0467	1	
33719_at	UNK AF0	AF010242	4	Pass	8.50	1.73	2	Fail	FALSE	TRUE	FALSE	3.00	2.83	protease, serine, 16 (thymus); PRSS16	6p21	
39306_at	PRSS16	AF052514	4	Pass	8.50	3.51	2	Fail	FALSE	TRUE	FALSE	3.00	2.83	heat shock protein, neuronal DNAJ-like 1; HSP1	2q32-q34	
37365_at	HSP1	X63368	4	Pass	7.75	2.22	4	Fail	FALSE	TRUE	FALSE	2.75	2.82	neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1); NCF1	7q11.23	
40951_at	UNK AL0	AL049250	5	Pass	6.40	5.50	3	Fail	FALSE	TRUE	FALSE	2.33	2.74	complement component 2; C2	6p21.3	
41351_at	UNK AAR	AA885106	4	Pass	26.25	7.85	6	Fail	FALSE	TRUE	FALSE	9.83	2.67	protein tyrosine kinase 2 beta; PTK2B	8p21.1	Kinase
35228_at	CPT1B	Y08682	5	Pass	9.60	2.88	5	Fail	FALSE	TRUE	FALSE	3.60	2.67	SREBP CLEAVAGE-ACTIVATING PROTEIN; SCAP	3	
40165_at	UNK ABC	AB015345	6	Pass	5.33	1.63	5	Fail	FALSE	TRUE	FALSE	2.00	2.67	Rab geranylgeranyltransferase, alpha subunit; RABGGTA	14q11.2	
40159_at	NCF1	M55067	6	Pass	70.83	\$2.24	5	Fail	FALSE	TRUE	FALSE	26.80	2.64	carnitine palmitoyltransferase I, muscle; CPT1B	22q13.33	
39837_s_at	UNK AC0	AC004877	4	Pass	14.50	8.74	4	Fail	FALSE	TRUE	FALSE	5.50	2.64	complement component 2; C2	6p21.3	
33374_at	C2	L09708	4	Pass	5.25	0.96	1	Fail	FALSE	TRUE	FALSE	2.00	2.63	protein tyrosine kinase 2 beta; PTK2B	8p21.1	Kinase
2009_at	PTK2B	U33284	4	Pass	5.25	1.50	2	Fail	FALSE	TRUE	FALSE	2.00	2.63	SREBP CLEAVAGE-ACTIVATING PROTEIN; SCAP	3	
41083_at	UNK AC0	AC006276	4	Pass	5.25	1.71	3	Fail	FALSE	TRUE	FALSE	2.00	2.63	Rab geranylgeranyltransferase, alpha subunit; RABGGTA	14q11.2	
37656_at	SCAP	D83782	5	Pass	11.00	3.94	4	Fail	FALSE	TRUE	FALSE	4.25	2.59	carnitine acetyltransferase; CRAAT	9q34.1	
100_g_at	RABGGTA	Y08200	5	Pass	9.40	4.16	3	Fail	FALSE	TRUE	FALSE	3.67	2.56	posmitotic segregation increased 2-like 11; PMS2L11	7q	
41648_at	CRAAT	X78706	4	Pass	20.50	3.11	4	Fail	FALSE	TRUE	FALSE	8.00	2.56	TATA box binding protein (TBP)-associated factor, RNA polymerase II, A, 250kD; TAF2A	14q13.1	
37977_at	PMS2L11	A1138834	4	Pass	7.25	3.30	6	Fail	FALSE	TRUE	FALSE	2.83	2.56	transmembrane activator and CAML interactor; TAC1		
37491_at	TAF2A	D90359	4	Pass	15.75	6.99	6	Fail	FALSE	TRUE	FALSE	6.17	2.55	lymphocyte antigen 6 complex, locus E; LY6E	8q24.3	
31410_at	TAC1	AF023614	4	Pass	7.00	4.08	4	Fail	FALSE	TRUE	FALSE	2.75	2.55	MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D); MEF2D	1q12-q23	
37360_at	LY6E	U66711	5	Pass	50.80	41.61	2	Fail	FALSE	TRUE	FALSE	20.00	2.54	Nei-associated factor 1; NAF1	5q32-q33.1	
35434_at	MEF2D	L16794	6	Pass	6.33	1.75	6	Fail	FALSE	TRUE	FALSE	2.50	2.53	Zxxin; ZYX	7q32	
38971_t_at	NAF1	AJ011896	4	Pass	53.50	25.51	5	Fail	FALSE	TRUE	FALSE	21.20	2.52	SH2 domain protein 2A; SH2D2A	1q21	
36958_at	ZYX	X95735	6	Pass	42.83	22.68	4	Fail	FALSE	TRUE	FALSE	17.00	2.52			
34432_at	SH2D2A	AF051325	5	Pass	4.60	3.71	6	Fail	FALSE	TRUE	FALSE	1.83	2.51			

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35194_at	GPX2	X53463	4	Pass	5.00	1.63	1	Fail	FALSE	TRUE	FALSE	2.00	glutathione peroxidase 2 (gastrintestinal); GPX2	14q24.1	
38276_at	NFKBIE	U91616	4	Pass	5.00	0.82	1	Fail	FALSE	TRUE	FALSE	2.00	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon		
40191_s_at	UNK_A170	A1761647	5	Pass	5.00	2.00	1	Fail	FALSE	TRUE	FALSE	2.00	KIAA0582 protein; KIAA0582	2	
35079_at	NB-3	AB003592	4	Pass	5.00	0.82	4	Fail	FALSE	TRUE	FALSE	2.00	contactin 6; CNTN6	3p26-p25	Phosphatase
36598_s_at	INPPL1	L36818	6	Pass	9.17	4.07	6	Fail	FALSE	TRUE	FALSE	3.67	inositol polyphosphate phosphatase-like 1; INPPL1	11q23	
35601_at	UNK_L000	L00022	6	Pass	16.83	9.47	6	Fail	FALSE	TRUE	FALSE	6.83			
37719_at	MLF2	AF070539	4	Pass	11.00	3.56	2	Fail	FALSE	TRUE	FALSE	4.50	myeloid leukemia factor 2; MLF2	12p13	
38464_at	GCS1	X87237	5	Pass	12.20	3.42	4	Fail	FALSE	TRUE	FALSE	5.00	glucosidase I; GCS1	2p13-p12	
40639_at	SCO2	AL021683	4	Pass	14.50	10.63	1	Fail	FALSE	TRUE	FALSE	6.00	SCO (cytochrome oxidase deficient, yeast) homolog 2; SCO2	22q13.33	
41273_at	UNK_AL0	AL040940	4	Pass	6.25	0.50	5	Fail	FALSE	TRUE	FALSE	2.60			
35961_at	UNK_AL0	AL049390	5	Pass	4.80	1.10	4	Fail	FALSE	TRUE	FALSE	2.00			
38721_at	HBP1	W72733	6	Pass	8.50	1.22	5	Fail	FALSE	TRUE	FALSE	3.60	HMG-box containing protein 1; HBP1	7q31.1	
519_g_at	NR1H2	U07132	6	Pass	25.17	7.57	3	Fail	FALSE	TRUE	FALSE	10.67	nuclear receptor subfamily 1, group H, member 2; NR1H2	19q13.3-19q13.3	
41127_at	SLC1A4	L14595	5	Pass	6.20	2.28	6	Fail	FALSE	TRUE	FALSE	2.67	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4; SLC1A4	2p15-p13	
38340_at	KIAA0655	AB014555	4	Pass	12.75	3.20	6	Fail	FALSE	TRUE	FALSE	5.50	huntingtin interacting protein-1-related; KIAA0655	12q24	
32177_s_at	GAPL	AC004084	4	Pass	9.25	2.22	2	Fail	FALSE	TRUE	FALSE	4.00	GTPase activating protein-like; GAPL	7q22-q31.1	
736_f_at	POM121L	D87002	4	Pass	10.00	2.58	3	Fail	FALSE	TRUE	FALSE	4.33			
1550_at	MAAT1	U19796	4	Pass	8.00	2.45	2	Fail	FALSE	TRUE	FALSE	3.50	melanoma-associated antigen recognised by T lymphocytes; MAAT1		*
37945_at	HBACH	U91316	4	Pass	6.25	1.71	4	Fail	FALSE	TRUE	FALSE	2.75	cytosolic acyl coenzyme A thioester hydrolase; HBACH	1p36.31-p36.11	
31822_at	CUTL1	L12579	5	Pass	9.40	3.29	6	Fail	FALSE	TRUE	FALSE	4.17	cut (Drosophila)-like 1 (CCAAT displacement protein); CUTL1	7q22	
33105_at	UNK_W28	W28790	4	Pass	5.25	2.63	3	Fail	FALSE	TRUE	FALSE	2.33			
35149_at	TNFRSF5	A1865431	4	Pass	6.75	3.59	6	Fail	FALSE	TRUE	FALSE	3.00	tumor necrosis factor receptor superfamily, member 5; TNFRSF5	20q12-q13.2	
40619_at	E2-EPF	M91670	4	Pass	8.50	1.00	6	Fail	FALSE	TRUE	FALSE	3.83	ubiquitin carrier protein; E2-EPF	17	
570_at	RELB	M83221	6	Pass	8.00	3.35	6	Fail	FALSE	TRUE	FALSE	3.67	v-rel avian reiculoendotheliosis viral oncogene homolog B (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3); RELB		
1007_s_at	DDR1	U48705	4	Pass	6.00	3.37	4	Fail	FALSE	TRUE	FALSE	2.75	discoidin domain receptor family, member 1; DDR1	6p21.3	Kinase
36856_at	UNK_W28	W28743	5	Pass	13.80	6.72	6	Fail	FALSE	TRUE	FALSE	6.33			

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37754_at	LGALS3B	L13210	4	Pass	3.25	1.50	4	Fail	FALSE	TRUE	FALSE	1.50	lectin, galactoside-binding, soluble, 3 binding protein (galactin 6 binding protein); LGALS3BP	17q25	
33387_at	GAS7	AB007854	4	Pass	6.00	1.83	5	Fail	FALSE	TRUE	FALSE	2.80	growth arrest-specific 7; GAS7	17p	
35960_at	IKBKB	AF031416	4	Pass	9.25	2.22	6	Fail	FALSE	TRUE	FALSE	4.33	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta; IKBKB	8p11.2	Kinase
40359_at	CTIORF13	M91083	5	Pass	19.20	4.09	4	Fail	FALSE	TRUE	FALSE	9.00	chromosome 11 open reading frame 13; CTIORF13	11p15.5	
1397_at	MAP3K11	L32976	4	Pass	4.25	1.50	3	Fail	FALSE	TRUE	FALSE	2.00	mitogen-activated protein kinase kinase 11; MAP3K11	11q13.1-q13.3	Kinase
33528_at	KIAA0125	D50915	4	Pass	4.25	0.96	3	Fail	FALSE	TRUE	FALSE	2.00	KIAA0125 gene product; KIAA0125		
38995_at	CLDN5	AF000959	4	Pass	14.00	3.74	5	Fail	FALSE	TRUE	FALSE	6.60	claudin 5 (transmembrane protein deleted in velocardiofacial syndrome); CLDN5	22q11.21	
39891_at	UNK_A12	A1246730	4	Pass	12.00	3.56	6	Fail	FALSE	TRUE	FALSE	5.67			
34669_at	TFE3	X96717	5	Pass	6.00	1.22	6	Fail	FALSE	TRUE	FALSE	2.83	transcription factor binding to IGHM enhancer	Xp11.22	Kinase
40925_at	UNK_AA5	AA554945	4	Pass	9.50	2.65	6	Fail	FALSE	TRUE	FALSE	4.50			
1000_at	MAPK3	X60188	6	Pass	7.33	3.08	6	Fail	FALSE	TRUE	FALSE	3.50	mitogen-activated protein kinase 3; MAPK3	16p11.2	Kinase
35763_at	UNK_AB0	AB011112	6	Pass	8.83	5.64	4	Fail	FALSE	TRUE	FALSE	4.25	KIAA0540 protein; KIAA0540		
41120_at	AMT	D14686	6	Pass	4.50	1.52	6	Fail	FALSE	TRUE	FALSE	2.17	aminomethyltransferase (glycine cleavage system protein T); AMT	3p21.2-p21.1	
703_at	UNK_L23	L23566	4	Pass	14.50	9.98	3	Fail	FALSE	TRUE	FALSE	7.00			
858_at	POR	S90469	4	Pass	7.75	3.30	4	Fail	FALSE	TRUE	FALSE	3.75	P450 (cytochrome) oxidoreductase; POR	7q11.2	
1089_i_at	UNK_M64	M64936	4	Pass	2.75	1.50	3	Fail	FALSE	TRUE	FALSE	1.33	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma; IKBKG	Xq28	
36004_at	IKBKG	AF074382	4	Pass	15.75	3.86	3	Fail	FALSE	TRUE	FALSE	7.67			
34868_at	KIAA1089	AB029012	5	Pass	4.60	1.14	4	Fail	FALSE	TRUE	FALSE	2.25	KIAA1089 protein; KIAA1089	1	
36184_at	PLOD	L06419	5	Pass	11.00	8.60	5	Fail	FALSE	TRUE	FALSE	5.40	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI); PLOD	1p36.3-p36.2	
39753_at	ITGA5	X06236	4	Pass	9.50	4.65	3	Fail	FALSE	TRUE	FALSE	4.67	Danlos syndrome type VI; integrin, alpha 5 (fibronectin receptor, alpha 5 polypeptide); ITGA5	12q11-q13	
36566_at	CTNS	AJ222967	4	Pass	4.00	1.41	1	Fail	FALSE	TRUE	FALSE	2.00	cystinosis, nephropathic; CTNS	17p13	
32562_at	ENG	X72012	4	Pass	8.00	2.71	3	Fail	FALSE	TRUE	FALSE	4.00	endoglin (Oster-Rendu-Weber syndrome 1); ENG	9q33-q34.1	
495_at	IL15RA	U31628	4	Pass	4.00	0.82	3	Fail	FALSE	TRUE	FALSE	2.00	interleukin 15 receptor, alpha; IL15RA	10p15-p14	
38020_at	KIAA0652	AB014552	5	Pass	4.80	2.39	5	Fail	FALSE	TRUE	FALSE	2.40	KIAA0652 gene product; KIAA0652	11	
40739_at	CA4	M83670	5	Pass	6.00	1.87	6	Fail	FALSE	TRUE	FALSE	3.00	carbonic anhydrase IV; CA4	17q23	
32802_at	TEB4	AB011169	6	Pass	8.67	4.50	6	Fail	FALSE	TRUE	FALSE	4.33	similar to S. cerevisiae SSM4; TEB4	5p15.2	

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38660_at	COX6A2	F27891	0	Fail	#DIV/0!	#DIV/0!	8	Pass	FALSE	FALSE	TRUE	2.63	cytochrome c oxidase subunit VIa polypeptide 2; COX6A2	16p	
32641_at	KIAA0979	AB023196	0	Fail	#DIV/0!	#DIV/0!	9	Pass	FALSE	FALSE	TRUE	2.56	protein, androgen-induced prostate proliferative shut-off associated protein; AS3, KIAA0979	13q12-q13.13q12.3	
32941_at	ICSBP1	M91196	0	Fail	#DIV/0!	#DIV/0!	9	Pass	FALSE	FALSE	TRUE	8.22	interferon consensus sequence binding protein 1; ICSBP1		
148_at	ELL2	U88629	1	Fail	11.00	#DIV/0!	7	Pass	FALSE	FALSE	TRUE	3.71	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR; ELL2		
35590_s_at	GIPR	X81832	3	Fail	25.33	2.89	7	Pass	FALSE	FALSE	TRUE	9.43	gastric inhibitory polypeptide receptor; GIPR	19q13.3	
31559_at	SLC13A2	U26209	3	Fail	11.67	2.08	7	Pass	FALSE	FALSE	TRUE	4.43	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2; SLC13A2	17p11.1-q11.1	
34903_at	UNK_A10	A1017382	3	Fail	15.67	7.09	9	Pass	FALSE	FALSE	TRUE	6.22	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (39kD); NDUFA9		
36205_at	NDUFA9	L04490	1	Fail	11.00	#DIV/0!	7	Pass	FALSE	FALSE	TRUE	4.43	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (39kD); NDUFA9	12p13.3	
32048_at	UNK_A10	AL049675	3	Fail	11.33	3.79	8	Pass	FALSE	FALSE	TRUE	4.63	nucleolar cysteine-rich protein; HSA6591		
37521_s_at	HSA6591	H82458	1	Fail	10.00	#DIV/0!	7	Pass	FALSE	FALSE	TRUE	4.14	nucleolar cysteine-rich protein; HSA6591		
396_f_at	EPOR	X97671	2	Fail	29.50	0.71	9	Pass	FALSE	FALSE	TRUE	12.44	erythropoietin receptor; EPOR	19p13.3-p13.2	
34098_f_at	UNK_A17	A1799757	2	Fail	7.50	2.12	7	Pass	FALSE	FALSE	TRUE	3.29	keratin, hair, acidic, 3A; KRTHA3A	17q12-q21	
31594_at	KRTHA3A	Y16788	2	Fail	11.00	5.66	7	Pass	FALSE	FALSE	TRUE	4.86	keratin, hair, acidic, 3A; KRTHA3A	17q12-q22	
40651_s_at	CRHR1	AF039523	1	Fail	7.00	#DIV/0!	10	Pass	FALSE	FALSE	TRUE	3.10	corticotropin releasing hormone receptor 1; CRHR1		
40299_at	RE2	AF091890	2	Fail	35.50	13.44	8	Pass	FALSE	FALSE	TRUE	15.75	G-protein coupled receptor; RE2		
33037_at	UNK_A10	AL022165	1	Fail	7.00	#DIV/0!	8	Pass	FALSE	FALSE	TRUE	3.13	sulfotransferase-2; C6ST-2	Xp11	
39920_r_at	CRF	AF095154	3	Fail	93.33	14.05	10	Pass	FALSE	FALSE	TRUE	41.70	CRF-related factor; CRF	17q21	
31586_f_at	UNK_X72	X72475	3	Fail	8.67	2.89	9	Pass	FALSE	FALSE	TRUE	3.89	farnesyltransferase, CAAAX box, beta; FNTB	14q23-q24	
37488_at	FNTB	L00635	2	Fail	7.00	1.41	7	Pass	FALSE	FALSE	TRUE	3.14	farnesyltransferase, CAAAX box, beta; FNTB	17q21	
2047_s_at	JUP	M23410	3	Fail	17.33	9.29	8	Pass	FALSE	FALSE	TRUE	7.88	junction plakoglobin; JUP	19p12	
888_s_at	GDF1	M62302	3	Fail	10.33	0.58	8	Pass	FALSE	FALSE	TRUE	4.75	growth differentiation factor 1; GDF1		
40622_r_at	UNK_A10	AL096740	3	Fail	38.00	13.11	9	Pass	FALSE	FALSE	TRUE	17.56	forkhead box M1; FOXM1	12p13	
41324_g_at	FOXM1	U90917	1	Fail	16.00	#DIV/0!	10	Pass	FALSE	FALSE	TRUE	7.50	forkhead box M1; FOXM1		
39844_at	UNK_A180	A1806379	2	Fail	8.00	2.83	12	Pass	FALSE	FALSE	TRUE	3.83	trinucleotide repeat containing 12; TNRC12	12qter	
34815_at	TNRC12	U80743	1	Fail	5.00	#DIV/0!	7	Pass	FALSE	FALSE	TRUE	2.43	trinucleotide repeat containing 12; TNRC12		
33493_at	HFL-EDD4	AF048849	2	Fail	10.00	2.83	8	Pass	FALSE	FALSE	TRUE	4.88	erythroid differentiation and demucation factor 1; HFL-EDD4		
1581_s_at	UNK_M27	M27504	1	Fail	5.00	#DIV/0!	9	Pass	FALSE	FALSE	TRUE	2.44	topoisomerase (DNA) II beta (180kD); TOP2B	3p24	
33697_at	P2RX7	Y12851	3	Fail	7.00	1.00	8	Pass	FALSE	FALSE	TRUE	3.50	purinergic receptor P2X, ligand-gated ion channel, 7; P2RX7	12q24	
31503_at	UNK_W28	W28732	2	Fail	9.50	7.78	11	Pass	FALSE	FALSE	TRUE	4.82			

HuPBMC_RA_U95A-Kin-PhosP.xls															
Affy Qualifier	Affy Name	accession	sum of Present Calls	4 of 6 present	Avg Freq RA	Std Dev RA	sum of abs dec	7 of 13 present	Present in RA and Normal	Present in RA, Absent in Normal	Absent in RA, Present in Normal	Fold Change RA / Normal	Name	Chromosome	Kinase or Phosphatase
718_at	PRSS11	D87258	2	Fail	4.50	0.71	7 Pass	FALSE	FALSE	FALSE	TRUE	1.97	protease, serine, 11 (IGF binding); PRSS11	10q25.3-q26.2	
38229_at	UNK_X90	X90579	3	Fail	92.33	20.98	7 Pass	FALSE	FALSE	FALSE	TRUE	1.96			
393_s_at	RUNX1	X90976	2	Fail	5.00	0.00	11 Pass	FALSE	FALSE	FALSE	TRUE	1.96	runt-related transcription factor 1 (acute myeloid leukemia 1; an11 oncogene); RUNX1	21q22.3	
1170_at	CSF1	M37435	1	Fail	9.00	#DIV/0!	10 Pass	FALSE	FALSE	FALSE	TRUE	1.96			
40490_at	DDX21	U41387	3	Fail	3.67	1.53	11 Pass	FALSE	FALSE	FALSE	TRUE	-2.13	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21; DDX21	#N/A 10	

Table 4

Table 4

CIA PBMC data															Fold changes are shown as normalized										TBS= total body score
TBS (0*)		Preart										TBS-7													
Systematic	Control	hrtic	TBS-1	TBS-3	TBS-4	TBS-5	TBS-6	TBS-9	Common	Genbank	EC	Description	Phenotype	Map	Keywords	Symbol									
J03023	0	-1.62	1.08	-3.25	2.23	1.54	1.54	1.62	hemopoietic cell kinase; Hck	J03023	2.7.1.112	TYROSINE-PROTEIN KINASE HCK (EC 2.7.1.112) (P56-HCK AND P60-HCK) (HEMOPOIETIC CELL KINASE) (B-CELL/MYELOID KINASE)	EXPRESSED PREDOMINANTLY IN CELLS OF THE MYELOID AND B-LYMPHOID LINEAGES.	2 86.0 cM	Hemostasis	Hck									
AA028657	0	3.00	19.00	17.00	17.00	37.50	16.50	20.00	EST; Unknown	AA028657					EST; Unknown	Unknown									
Msa.10146.0	0	1.80	12.40	13.80	13.60	19.60	15.20	19.20	vWF, human	AA168633					Hemostasis										
Msa.10146.0	0	1.80	12.40	13.80	13.60	19.60	15.20	19.20	vWF, human	AA168633					Hemostasis										
W62701	0	2.40	20.20	19.00	16.40	22.80	18.20	18.80		W62701															
W62701	0	2.40	20.20	19.00	16.40	22.80	18.20	18.80		W62701															
Msa.1497.0	0	1.50	7.00	5.50	6.00	11.00	6.50	15.50	calmodulin 3; Calm3	M19380	2.7.1.38			7 4.0 cM	Regulatory	Calm3									
Msa.1497.0	0	1.50	7.00	5.50	6.00	11.00	6.50	15.50	calmodulin 3; Calm3	M19380	2.7.1.38			7 4.0 cM	Regulatory	Calm3									
Msa.723.0	0	2.00	8.00	5.00	3.00	10.00	9.00	15.00	aquaporin 1; Aqp1	L02914		AQUAPORIN-CHIP (WATER CHANNEL PROTEIN FOR RED BLOOD CELLS AND KIDNEY PROXIMAL TUBULE) (AQUAPORIN 1) (EARLY RESPONSE	ERYTHROCYTES AND RENAL TUBULES.	6 27.0 cM	Cell Surface Protein	Aqp1									
D16262	0	0.00	9.00	10.00	8.00	21.00	16.00	14.00	mesoderm specific transcript; Mest	D16262				6 7.5 cM	Cytokine	Mest									

Table 1. Summary of the data for the CTLA-2-BETA protein precursor (FRAGMENT) and its precursors.

X15592	0	1.33	13.67	13.00	16.67	14.67	13.00	14.00	cytotoxic T lymphocyte-associated protein 2 beta; Ctla2b	X15592		CTLA-2-BETA PROTEIN PRECURSOR (FRAGMENT)		13 42.0 cM		Ctla2b
Msa.3237.0	0	0.00	7.50	9.00	9.00	9.50	9.50	13.50	four and a half LIM domains 1; Fhl1	W14830				X A6-A7.1	Regulatory	Fhl1
M87276	0	0.00	6.00	7.00	5.00	10.00	11.00	13.00	thrombospondin 1; Thbs1	M87276		THROMBOSPONDIN 1 PRECURSOR.		2 65.0 cM	Extracellular Protein	Thbs1
AA616664	0	0.00	10.75	11.00	10.00	16.75	12.00	11.25		AA616664						
W45778	0	1.27	8.47	9.40	9.00	9.53	8.00	9.27	von Willebrand Factor; vWF; homolog	W45778					Hemostasis	vWF
W64688	0	0.00	6.82	7.36	5.55	9.82	7.09	8.73		W64688					EST; Unknown	
ab000822	0	1.10	7.30	7.10	7.80	10.10	7.70	8.50	synaptosomal-associated protein, 23kD; Snap23	AB000822				2 61.8 cM		Snap23
M19380	0	0.00	4.67	4.00	5.33	9.00	6.67	8.33	calmodulin 3; Calm3	M19380	2.7.1.38			7 4.0 cM	Regulatory	Calm3
AA542220	0	-1.09	5.00	4.75	7.00	8.92	5.92	7.50	TBX1 protein; TBX1	AA542220		TBX1 PROTEIN (T-BOX PROTEIN 1) (TESTIS-SPECIFIC T-BOX	TESTIS SPECIFIC.		Intracellular Protein	TBX1
Msa.1160.0	0	0.00	7.67	2.00	7.67	2.00	5.33	5.67	serum amyloid A 3; Saa3	X03505		SERUM AMYLOID A-3 PROTEIN PRECURSOR.	FOUND IN VARIOUS TISSUES.	7 23.5 cM	Extracellular Protein	Saa3
X03479	0	-1.20	6.17	1.50	5.17	1.67	3.50	5.17	serum amyloid A 3; Saa3	X03479		SERUM AMYLOID A-3 PROTEIN PRECURSOR.	FOUND IN VARIOUS TISSUES.	7 23.5 cM	Extracellular Protein	Saa3
U92478	0	0.00	3.00	2.33	3.33	6.00	5.33	4.67	development and differentiation enhancing; Ddef1	U92478					Regulatory	Ddef1

Table 1. Gene expression data for the 143 genes

Msa.3665.0	0	-1.12	3.33	4.00	3.67	5.44	4.67	4.67	DNA segment, Chr 2, Wayne State University 143, expressed; D2Wsul43e	AA116604					2 24.0 cM	Proteolytic	D2Wsul43e
D67016	0	-2.33	-1.75	-1.75	1.14	3.14	1.14	4.43	heat shock protein, 105 kDa; Hsp105	D67016			HEAT-SHOCK PROTEIN 105 KDA (HEAT SHOCK-RELATED 100 KDA PROTEIN E7I) (HSP-E7I) (HEAT SHOCK 110 KDA PROTEIN) (42.2)	FOUND IN MOST TISSUES. HIGHLY EXPRESSED IN BRAIN.	5 88.0 cM		Hsp105
AA120653	0	-1.69	2.84	2.41	2.77	4.50	3.07	3.80	transgelin 2; Tagln2	AA120653					1 94.2 cM	Structural Protein	Tagln2
AA285502	0	-2.00	2.00	2.00	2.00	4.50	3.50	3.75	receptor (calcitonin) activity modifying protein 1; Ramp1	AA285502						Regulatory	Ramp1
U35124	0	-1.87	2.07	2.00	2.27	4.00	2.73	3.67	protein tyrosine phosphatase, non-receptor type 18; Ptpn18	U35124					1 17.3 cM	Regulatory	Ptpn18
U05837	0	-1.60	0.00	-1.14	1.75	2.25	2.00	3.50	hexosaminidase A; Hexa	U05837			BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL-BETA-GLUCOSAMINIDASE) (BETA-N-ACETYLHEXOSAMINIDASE)		9 29.0 cM	Proteolytic	Hexa

Table 1. The data of the

U27830	0	-1.67	-2.50	-2.50	0.00	2.00	1.20	3.20	stress-induced phosphoprotein 1; Stip1	U27830							Stip1
Msa.4113.0	0	-1.50	1.44	1.22	2.78	1.33	2.44	3.11	glucocorticoid-induced leucine zipper; Gilz	AA050733							Gilz
C79010	0	-1.33	2.25	2.08	4.33	4.25	3.00	3.08	Src-associated adaptor protein; Saps	C79010						??	Saps
C79010	0	-1.33	2.25	2.08	4.33	4.25	3.00	3.08	Src-associated adaptor protein; Saps	C79010						??	Saps
Msa.16995.0	0	-1.27	2.79	2.64	5.29	3.07	2.57	3.04	arachidonate 5-lipoxygenase activating protein	W83564						Intracellular Protein	
M22479	0	-2.00	2.75	3.00	3.00	5.00	3.50	3.00	tropomyosin 2, beta; Tpm2	M22479						EST; Unknown	Tpm2
AA238483	0	-3.33	-2.00	-2.00	-1.25	-1.11	-1.11	2.90	CD8 antigen, beta chain; Cd8b	AA238483			T-CELL SURFACE GLYCOPROTEIN CD8 BETA CHAIN PRECURSOR (T-CELL SURFACE GLYCOPROTEIN LYT-3) (T-CELL MEMBRANE GLYCOPROTEIN)		6 30.5 cM		Cd8b
M27960	0	-2.00	1.17	-2.00	3.50	1.33	1.33	2.83	interleukin 4 receptor, alpha; Il4ra	M27960			INTERLEUKIN 4 RECEPTOR ALPHA CHAIN		7 62.0 cM	Receptor	Il4ra
AA033103	0	-1.33	1.75	1.50	2.75	3.25	1.50	2.75		AA033103							
AA261246	0	-1.47	2.71	2.61	4.14	4.57	2.89	2.71		AA261246							
AA104254	0	-6.00	-6.00	-6.00	-3.00	-6.00	-1.20	2.67	transcription factor 17; protein kinase KID-1 (kinase induced by depolarization); rat	AA104254						Transcription Factor	KID-1

Table 1. Summary of protein properties and functions.

AA123934	0	-2.67	-2.00	-4.00	0.00	1.38	1.25	2.38	EST; Unknown	AA123934								EST; Unknown	Unknown
L28177	0	-1.20	2.17	2.33	4.50	2.83	2.67	2.33	DNA-damage inducible transcript 1; Ddit1; (GADD45a)	L28177				GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN	3 70.5 cM		Intracellular Protein	Ddit1	
Msa.641.0	0	-1.49	2.11	1.91	3.47	2.27	1.92	2.31	Fc receptor, IgE, high affinity I, gamma polypeptide; Fcrlg	W41745				HIGH AFFINITY IMMUNOGLOBULIN RECEPTOR GAMMA-SUBUNIT PRECURSOR (FCER1) (IGE FC RECEPTOR, GAMMA-SUBUNIT) (FC-EPSILON)	1 93.3 cM		Receptor	Fcrlg	
AA033074	0	-1.43	2.30	1.40	3.10	3.10	1.70	2.30	flotillin 1; Flotl	AA033074								Flotl	
U73004	0	-1.14	1.91	2.18	3.48	3.06	2.27	2.15	secretory leukocyte protease inhibitor; Slpi	U73004				ANTILEUKOPROTEINASE 1 PRECURSOR (ALP) (SECRETORY LEUKOCYTE PROTEASE INHIBITOR). HIGHEST EXPRESSION IN LUNG, SPLEEN, INTESTINE AND EPIDIDYMIS WITH LOWER LEVELS IN LIVER AND SEMINAL VESICLE. NO EXPRESSION IN BRAIN, HEART, KIDNEY AND			Proteolytic	Slpi	

D37837	0	-1.20	0.00	-1.29	3.39	1.28	1.39	2.06	plastin 2, L; Pls2	D37837		L-PLASTIN (LYMPHOCY TE CYTOSOLIC PROTEIN 1) (LCP-1) (65 KDA MACROPHAG E PROTEIN)				Pls2
X81627	0	1.43	4.86	3.14	17.29	3.14	2.14	2.00	lipocalin 2; Lcn2	X81627		NEUTROPHIL GELATINASE- ASSOCIATED LIPOCALIN PRECURSOR (NGAL) (P25) (SV-40 INDUCED 24P3		2 27.0 cM		Lcn2
Msa.2129.0	0	2.00	6.33	3.67	31.67	3.33	2.00	2.00	lipocalin 2; Lcn2	W13166		NEUTROPHIL GELATINASE- ASSOCIATED LIPOCALIN PRECURSOR (NGAL) (P25) (SV-40 INDUCED 24P3		2 27.0 cM		Lcn2
U96687	0	0.00	1.47	-1.25	3.07	1.73	1.53	2.00	paired-Ig-like receptor A10,paired-Ig- like receptor A6; Pira10,Pira6	U96687						Pira10,Pira6
U27838	0	-3.50	-1.40	-3.50	0.00	1.57	1.29	2.00	GPI-anchored membrane protein 1; Gpiap-pending	U27838						Gpiap-pending
Msa.3234.0	0	-1.33	-2.00	-4.00	2.75	1.25	0.00	2.00	myosin If; Myo1f	X97650				17 17.5 cM		Myo1f
AA032906	0	-9.00	-9.00	-9.00	-4.50	-1.50	-1.29	2.00	Homologous to GENESEQN:V 49566 (human)	AA032906						Patented; Novel
AA032906	0	-9.00	-9.00	-9.00	-4.50	-1.50	-1.29	2.00	Homologous to GENESEQN:V 49566 (human)	AA032906						Patented; Novel

Table 1. Gene expression data

AA271024	0	-4.00	-4.00	-6.00	-1.33	1.08	-1.09	1.92	small nuclear ribonucleoprotein D2 (SNRPD2)	AA271024						Other	
Msa.31660.0	0	-1.58	1.37	1.07	3.07	1.20	1.53	1.87	CD53 antigen; Cd53	AA105582					3 50.5 cM	Cell Surface Protein	Cd53
ET62056	0	-3.22	-1.76	-2.32	1.45	1.29	1.33	1.86	immunoglobulin rearranged kappa chain	ET62056						Extracellular Protein	
ab009287	0	-2.33	-3.50	-7.00	0.00	1.14	0.00	1.86	CD68 antigen; Cd68	AB009287				EXPRESSED IN TISSUE MACROPHAGES AND TO A LESSER EXTENT IN DENDRITIC CELLS.	11 39.0 cM	Cell Surface Protein	Cd68
AA241085	0	-4.00	1.17	1.08	1.42	2.08	1.67	1.83	GENESEQN:Z 34468 Mouse 15 kDa selenoprotein	AA241085							
AA020104	0	-3.25	-1.62	-1.30	1.23	1.62	1.23	1.77	glycosylation dependent cell adhesion molecule 1; Glycam I	AA020104				SULFATED 50 KDA GLYCOPROTEIN PRECURSOR (SGP50) (ENDOTHELIAL LIGAND FOR L- SELECTIN) (GLYCOSYLATION- DEPENDENT CELL ADHESION MOLECULE	15 63.0 cM		Glycam I
Msa.38664.0	0	-2.13	-1.06	-1.89	4.88	1.12	1.06	1.76		AA144469						EST; Unknown	

Table 1

X94353	0	-1.33	3.00	2.25	5.50	1.75	1.75	1.75	1.75	1.75	catheлин-like protein; Cnlp	X94353		CATHELIN-RELATED ANTIMICROBIAL PEPTIDE PRECURSOR (CRAMP) (CATHELIN-LIKE PROTEIN) (CLP).	EXPRESSED IN TESTIS, SPLEEN, STOMACH, AND INTESTINE. VERY LOW EXPRESSION FOUND IN HEART, LUNG AND SKELETAL MUSCLE. NO EXPRESSION IN BRAIN, KIDNEY OR LIVER.	9 61.0 cM	Metabolic	Cnlp
ET62844	0	-1.33	1.25	-1.33	3.13	1.75	1.38	1.75	1.75	1.75	paired-Ig-like receptor A10, paired-Ig-like receptor A6; Pira10, Pira6	ET62844				7	Receptor	Pira10, Pira6
U06119	0	-2.88	-1.64	-3.29	1.17	1.35	1.26	1.74	1.26	1.74	cathepsin H; Cish	U06119	3.4.22.16	CATHEPSIN H PRECURSOR WITH HIGHEST EXPRESSION FOUND IN NON-SKELETAL TISSUES. LOW LEVELS FOUND IN SKELETAL TISSUE.	WIDELY EXPRESSED WITH HIGHEST EXPRESSION FOUND IN NON-SKELETAL TISSUES. LOW LEVELS FOUND IN SKELETAL TISSUE.	9 50.0 cM	Proteolytic	Cish
M35153	0	-1.75	1.29	1.29	3.71	1.71	2.00	1.71	2.00	1.71	lamin B1; Lmnb1	M35153		LAMIN B1.		18 29.0 cM	ECM (Matrix Prot)	Lmnb1
Msa.739.0	0	-1.04	2.08	1.17	5.63	1.79	1.33	1.71	1.33	1.71	haptoglobin; Hp	M96827				8 55.0 cM	Extracellular Protein	Hp
AA445408	0	-5.00	-2.50	-10.00	-1.43	-1.43	1.20	1.70	1.20	1.70	H3 histone, family 3B; H3Bb	AA445408					Other	H3Bb

*

Table 1. Genes and proteins involved in the DNA damage response pathway.

Msa.7498.0	0	-1.50	1.67	1.33	0.00	3.67	1.33	1.67	1.33	1.67	growth arrest and DNA-damage-inducible, gamma; Gadd45g	AA138777		GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD45 GAMMA (CYTOKINE RESPONSIVE			Regulatory	Gadd45g
Msa.1903.0	0	-3.63	-2.07	-4.83	1.03	-1.61	-1.38	1.66			histocompatibility 2, class II, locus DMa,histocompatibility 2, class II, locus Mb1,histocompatibility 2, class II, locus Mb2,proteosome (prosome, macropain) subunit, beta type 9 (large multifunctional protease 2); H2-DMa,H2-DMb1,H2-DMb2,Psb9	U35323		CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR, CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA 1 CHAIN PRECURSOR (H2-M BETA 1 CHAIN),PROTEASOME CHAIN 7 PRECURSOR (EC 3.4.99.46) (MACROPAIN CHAIN 7) (MULTICATALYTIC ENDOPEPTIDASE	17 18.56 cM,17 18.57 cM,17 18.58 cM,17 18.59 cM	<input type="checkbox"/>	H2-DMa,H2-DMb1,H2-DMb2,Psb9	
U96689	0	-1.06	1.59	1.29	3.18	1.94	1.65	1.65			paired-Ig-like receptor B; Pirb	U96689				7 1.0 cM	Receptor	Pirb
V01527	0	-3.55	-1.95	-4.33	0.00	-1.30	-1.11	1.62			histocompatibility 2, class II antigen A, beta 1; H2-Ab1	V01527		H-2 CLASS II HISTOCOMPATIBILITY ANTIGEN, A-D BETA CHAIN	17 18.64 cM		Cell Surface Protein	H2-Ab1
AA285691	0	-3.29	-1.55	-2.32	1.37	1.37	1.01	1.61			cytohesin binding protein (Cbp)	AA285691					Cell Surface Protein	

Table 1. Myd116 protein properties

Accession	Gene	Protein	Length (aa)	Weight (kDa)	PI	Charge	Hydropathy	Instability	Stability	Function	Location	Other	Myd116
X51829	myeloid differentiation primary response gene 116; Myd116		1.60		-1.11	-1.25	-1.25	-3.33	-2.50	-5.00	0		
AA185060	GENESEQ:Z AA185060 52941 Human prostate tumor cDNA library derived EST fragment #84		1.57		0.00	1.29	0.00	-2.33	-2.33	-3.50	0	Unknown	
U59488	neutrophil cytosolic factor 4; Ncf4		1.57		0.00	-1.17	1.43	-3.50	-2.33	-1.75	0	Intracellular Protein	Ncf4
L37297	neutrophilic granule protein; Ngp		1.50		2.00	2.50	20.75	2.00	3.00	-2.00	0	Intracellular Protein	Ngp
L37297	neutrophilic granule protein; Ngp		1.50		2.00	2.50	20.75	2.00	3.00	-2.00	0	Intracellular Protein	Ngp
D73368	enhancer of rudimentary homolog (Drosophila); Erh		1.50		0.00	1.08	-1.20	-6.00	-3.00	-4.00	0	Other	Erh
K01923	histocompatibility 2, class II antigen A, alpha; H2-Aa		1.50		1.03	1.04	-1.14	-2.92	-1.54	-3.75	0	Cell Surface Protein	H2-Aa

Table 1. Enzymes and their substrates in the plasma and platelet.

Msa.1700.0	0	-1.37	1.36	-1.29	3.14	1.32	1.09	1.45	phospholipase A2 group VII (platelet-activating factor acetylhydrolase, plasma); Pla2g7	U34277	3.1.1.47	PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47) (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE	PLASMA.	Cytokine	Pla2g7
C76739	0	-1.29	1.33	1.33	3.44	2.11	1.78	1.44	macrophage C-type lectin; Mpel	C76739				Cell Surface Protein	Mpel
U29947	0	-2.29	-1.78	-4.00	1.44	1.19	1.13	1.44	mannosidase 2, alpha B1; Man2b1	U29947		LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (EC 3.2.1.24) (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID		Regulatory	Man2b1

*

Table 1

AA008321	0	-1.75	-1.75	-3.50	1.43	1.86	0.00	1.43	proteasome (prosome, macropain) subunit, alpha type 4; Psm4	AA008321	3.4.99.46	PROTEASOM E COMPONENT C9 (EC 3.4.99.46) (MACROPAIN SUBUNIT C9) (MULTICATALYTIC ENDOPEPTIDASE)			Proteolytic	Psm4
T25659	0	-3.50	-1.40	-2.33	1.14	1.14	0.00	1.43	heterogeneous nuclear ribonucleoprotein A2/B1; Hmpa2b1	T25659		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1 (HNRNP A2)			EST; Unknown	Hmpa2b1
AA638408	0	-3.40	-2.83	-4.25	-1.42	-1.31	-1.13	1.41	arginine N-methyltransferase 1; Mirm1	AA638408					Signal Transduction	Mirm1
AA408475	0	-3.33	-2.50	-2.50	-1.11	1.50	1.30	1.40	ribosomal protein L13a; Rpl13a	AA408475		60S RIBOSOMAL PROTEIN L13A (TRANSPLANTATION ANTIGEN P198) (TUM-PI98)	7 25.0 cM		Intracellular Protein	Rpl13a
M59378	0	-3.25	-1.86	-3.25	-1.18	1.08	-1.30	1.38	tumor necrosis factor receptor superfamily, member 1b; Tnfrsf1b	M59378		TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75)	4 75.5 cM		Receptor	Tnfrsf1b
AA189914	0	-1.26	2.08	2.83	2.79	3.92	2.38	1.38	cytidine monophosphate-N-acetylneuraminic acid synthetase; Cmas	AA189914			6 74.0 cM			Cmas
AA261402	0	-2.78	-1.92	-3.57	1.04	1.24	-1.14	1.36	EST; Unknown	AA261402					EST; Unknown	Unknown



Coronin-like protein p57 (Coronin 1A)

AA174982	0	-2.37	-1.76	-3.10	1.17	1.11	-1.17	1.36	coronin, actin binding protein 1A; Corola	AA174982		CORONIN-LIKE PROTEIN P57 (CORONIN 1A)		7 62.5 cM	Intracellular Protein	Corola
AA182228	0	-2.56	-3.29	-7.67	-1.15	-1.21	-1.28	1.35	EST; Unknown	AA182228					EST; Unknown	Unknown
AF032466	0	-1.50	2.33	1.67	6.00	2.33	1.33	1.33	arginase type II; Arg2	AF032466	3.5.3.1	ARGINASE II PRECURSOR (EC 3.5.3.1) (NON-HEPATIC ARGINASE) (KIDNEY-TYPE				Arg2
AA152590	0	-3.00	-2.25	-4.50	-1.29	1.44	1.11	1.33	eukaryotic translation initiation factor 4A1; Eif4a1	AA152590			11 39.0 cM	Translation Factor		Eif4a1
AA273932	0	-3.57	-2.08	-2.78	-1.19	1.08	-1.09	1.32	aldo-keto reductase; LOC56043	AA273932				Other		LOC56043
AA189758	0	-3.25	-1.86	-3.25	-1.18	1.08	1.15	1.31	Wbscr5 gene product; Wbscr5	AA189758				Regulatory		Wbscr5
Msa.4530.0	0	-2.88	-1.92	-3.83	0.00	-1.15	-1.15	1.30	EST; region of homology to GENESEQN:Z 77537 Human ovarian tumor cDNA library derived EST fragment 88	AA106931				EST; Unknown		
K01925	0	-3.84	-1.66	-3.31	-1.16	-1.10	-1.10	1.30	histocompatibility 2, class II antigen A, alpha; H2-Aa	K01925		H-2 CLASS II HISTOCOMPATIBILITY ANTIGEN, A-K ALPHA CHAIN	17 18.65 cM	Hemostasis		H2-Aa

Table 1. List of genes and proteins identified in the microarray analysis of the Msa.928.0 strain.

Msa.928.0	0	-1.60	1.38	0.00	3.50	1.38	1.13	1.13	1.13	myristoylated alanine rich protein kinase C substrate; Macs	M60474	MYRISTOYL ATED ALANINE- RICH C- KINASE SUBSTRATE (MARCKS).	BRAIN, SPLEEN, LESS IN KIDNEY AND HEART, AND VERY LOW LEVELS IN	10 22.0 cM	Structural Protein	Macs
AA020128	0	-4.50	-3.00	-3.00	1.33	1.44	1.11	1.11	1.11		AA020128					
U91848	0	-5.00	-2.22	-4.00	-1.43	-1.33	0.00	1.10	1.10	clathrin, light polypeptide (Lca); Cita	U91848	CLATHRIN LIGHT CHAIN A.			Structural Protein	Cita
U16985	0	-3.12	-3.00	-4.26	-1.19	-1.09	-1.31	1.05	1.05	lymphotoxin B; Ltb	U16985	LYMPHOTOX IN-BETA (LT- BETA) (TUMOR NECROSIS FACTOR C).		17 19.06 cM	Cytokine	Ltb
Z27231	0	-1.17	2.00	0.00	5.86	1.71	1.29	0.00	0.00	matrix metalloprotein ase 9; Mmp9	Z27231	92 KDA TYPE IV COLLAGENA SE PRECURSOR (EC 3.4.24.35) (92 KDA GELATINASE (MATRIX METALLOPR OTEINASE-9) (MMP-9) (GELATINAS		2 96.0 cM	Metabolic	Mmp9
D17630	0	-1.20	1.83	0.00	4.50	1.83	1.33	-1.20	-1.20	chemokine (C- X-C) receptor 2; Cmkar2	D17630	HIGH AFFINITY INTERLEUKI N-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA		1 40.0 cM		Cmkar2

Table 1: Targeted

AA407584	0	-4.00	-2.00	-3.00	-2.00	-1.09	-1.33	-1.20	DNA segment, Chr 7, Wayne State University 30, expressed,nucl eosome assembly protein 1-like 4; D7Wsu30c,Na p114	AA407584					7 69.0 cM,7 69.55 cM		D7Wsu30e
AA529094	0	-3.33	-2.50	-3.33	-1.43	-1.25	-1.11	-1.25		AA529094							
X93037	0	-1.50	-1.50	-1.50	3.33	0.00	-1.50	-1.50	extracellular proteinase inhibitor; Expi	X93037		WDNM1 PROTEIN PRECURSOR.					Expi
M22326-2	0	-6.00	-4.40	-11.00	-6.00	-2.64	-3.88	-1.69	early growth response 1; Egr1	M22326		EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (KROX-24 PROTEIN)		18 16.0 cM	Intracellular Protein	Egr1	

Table 5

CIA-001,011,012pawsU-FC Raw data from GEDS Fold Change, Genes were originally filtered for Present/Absent using frequency data

Note here

Note here

Score (0*)

Systematic

	control		prearth		Score 1		Score 2		Score 3		Score 4	
	Raw	P	Raw	I	Raw	StdErr	Raw	StdErr	Raw	StdErr	Raw	StdErr
D37801	1.00	-1.13	-2.72	0.68	-1.99	0.15	-2.79	0.82	-2.51	0.14		
AA204199	1.00	2.86	-3.91	2.24	-0.03	1.37	-2.26	0.12	-2.68	0.30		
U28244	1.00	-1.70	-1.41	1.43	-0.79	1.88	-6.34	2.53	-6.56	1.87		
Msa.30443.0	1.00	1.21	2.19	0.78	2.28	0.60	9.18	1.92	11.29	3.33		

Common	Genbank	description	function	Map	Keywords	Kinase or Phosphatase
protein tyrosine phosphatase, non-receptor type 21; Ptpn21	D37801	protein tyrosine phosphatase, non-receptor type 21 (ec 3.1.3.48) (protein-tyrosine phosphatase ptp-d110)	may be involved in the regulation of growth and differentiation of liver cells.			Phosphatase
protein tyrosine phosphatase 4a3; Ptp4a3	AA204199		northern blot analysis revealed that prt-2 is preferentially expressed in skeletal muscle, while prt-3 is preferentially expressed in both skeletal muscle and heart, although both prt-2 and prt-3 are expressed at lower levels in other tissues.		Signal Transduction	Phosphatase
phospholipase A2, group IIA (platelets, synovial fluid); Pla2g2a	U28244	phospholipase a2, membrane associated precursor (ec 3.1.1.4) (phosphatidylcholine 2-acylhydrolase) (group ii phospholipase a2) (enhancing factor)	pa2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.	4 68.0 cM		Phosphatase
RAS-related C3 botulinum substrate 2; Rac2	AA097231	ras-related c3 botulinum toxin substrate 2 (p21-rac2) (en-7 protein)	function: seems to be involved in the regulation of the nadph oxidase. subcellular location: cytoplasmic; membrane-associated when activated. tissue specificity: hematopoietic specific. similarity: belongs to the small		Intracellular Protein	Kinase

Table 1. Summary of protein data bank (PDB) entries for the protein kinase A (PKA) family.

J03023	1.00	-1.22	0.45	0.71	0.96	2.17	3.77	0.26	4.24	0.44	hemopoietic cell kinase; Hck	J03023	tyrosine-protein kinase hck (ec 2.7.1.112) (p56-hck and p60-hck) (hemopoietic cell kinase) (b- cell/myeloid kinase) (bmk).	may serve as part of a signaling pathway coupling the receptor to the activation of the respiratory burst. may also contribute to neutrophil migration and may regulate the degranulation process of neutrophils.	286.0 cM	Hemostasis	Kinase	*
X06368	1.00	-2.02	-2.80	1.36	-0.30	1.81	1.50	0.23	1.45	0.19	colony stimulating factor 1 receptor; Csflr	X06368	macrophage colony stimulating factor 1 receptor precursor (csf-1-r) (ec 2.7.1.112) (fms proto-oncogene) (c-fms).	this protein is the receptor for csf-1, it is a protein tyrosine-kinase transmembrane receptor.	1830.0 cM	Cytokine	Kinase	*
Msa.1709.0	1.00	-1.81	-3.77	0.76	-1.37	2.51	-1.58	0.33	0.10	0.93	elastin; Eln	U08210	elastin precursor (tropoelastin).	major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover completely.	575.0 cM		Kinase	*
Msa.6386.0	1.00	1.42	-3.46	2.04	-1.35	0.22	-2.64	0.72	-3.21	0.57	mitogen activated protein kinase 13; Mapk13	W13523			17 A3-B		Kinase	*
Msa.11160.0	1.00	1.00	17.56	13.65	12.86	11.86	106.21	7.39	107.32	28.80	serum amyloid A 3; Saa3	X03505	serum amyloid a-3 protein precursor.	member of "a family of apolipoproteins that are differentially expressed. some represent acute phase proteins in the response to inflammatory stimuli. one acts as a precursor of the amyloid a protein, a major constituent of amyloid plaques.	723.5 cM	Extracellular Protein		*

Table 1. Serum amyloid A (SAA) and serum amyloid A3 (SAA3) protein families

Accession	1.00	-1.29	13.98	9.47	18.92	17.89	104.27	16.64	92.13	20.20	Serum amyloid A 3; Saa3	X03479	Serum amyloid a-3 protein precursor.	Serum amyloid a proteins (saa) constitute a family of apolipoproteins that are differentially expressed. some family members represent acute phase proteins in the response to inflammatory stimuli. one of these acts as a	7 23.5 cM	Extracellular Protein	*
X03479																	
U73004	1.00	4.48	15.01	7.85	9.35	4.84	56.63	17.17	86.24	20.61	secretory leukocyte protease inhibitor; Sipi	U73004	antileukoproteinase 1 precursor (alp) (secretory leukocyte protease inhibitor).	acid-stable proteinase inhibitor with strong affinities for trypsin, chymotrypsin, elastase, and cathepsin g. may prevent elastase-mediated damage to oral and possibly other mucosal tissues. associated with wound healing due to its inhibition of		Proteolytic	*
M83219	1.00	8.84	25.35	7.26	17.08	10.37	45.22	2.88	62.94	10.24	S100 calcium-binding protein A9 (calgranulin B); S100a9	M83219	calgranulin b (migration inhibitory factor-related protein 14) (mrp-14) (p14) (leukocyte 11 complex heavy chain).	expressed by macrophages in acutely inflamed tissues and in chronic inflammations. seems to be an inhibitor of protein kinases. also expressed in epithelial cells constitutively or induced during dermatoses. may interact with	3 43.6 cM	Cytokine	*
U27267	1.00	1.00	9.77	7.32	6.29	5.29	46.55	3.12	52.23	16.41	small inducible cytokine B subfamily, member 5; Scyb5	U27267	small inducible cytokine b5 precursor (cytokine lix).	may participate in the recruitment of inflammatory cells by injured or infected tissue. involved in neutrophil activation	5 53.0 cM	Cytokine	*

Table 1. Properties of lipocalin 2 and lipocalin 9

Msa.2129.0	1.00	2.49	9.94	3.74	4.24	3.09	49.39	3.66	45.88	11.97	lipocalin 2; Lcn2	W13166	neutrophil gelatinase-associated lipocalin precursor (ngal) (p25) (sv-40 induced 24p3 protein).	acute phase forms a covalently linked, disulfide-bridged heterodimer with the 92 kd type v collagenase (mmp-9). neutrophil gelatinase-associated lipocalin 2,25kda, found at moderate levels, only in breast and lung, component of human tear (lipophilic ligand carrier protein suprefamily, lipocalin family, kemal group), modulator of inflammation, involved in the	2 27.0 cM	Extracellular Protein	
J04596	1.00	1.16	6.78	5.34	3.06	1.86	25.23	2.49	37.61	11.33	GRO1 oncogene; Gro1	J04596	growth regulated protein precursor (platelet-derived growth factor-inducible protein kc) (secretory protein n51).	has chemotactic activity for neutrophils. contributes to neutrophil activation during inflammation (bv similariv)	5 51.0 cM	Extracellular Protein	
Z27231	1.00	2.87	3.52	2.37	10.54	8.59	22.63	6.04	32.08	4.73	matrix metalloproteinase 9; Mmp9	Z27231	92 kda type iv collagenase precursor (ec 3.4.24.35) (92 kda gelatinase) (matrix metalloproteinase-9) (mmp-9) (gelatinase b) (gelb).	regulator in matrix remodeling, expressed in alveolar macrophages and granulocytes, key regulator of growth plate angiogenesis and apoptosis of hypertrophic chondrocytes in mice, and involved in the	2 96.0 cM	Metabolic	
M15131	1.00	1.55	5.35	3.53	5.53	4.53	28.75	3.16	31.62	8.61	interleukin 1 beta; Il1b	M15131	interleukin-1 beta precursor (il-1 beta).	produced by macrophages and monocytes, it is required for the interaction between antigen-presenting cells and lymphocytes initiating an immune response. it can also be produced from a number of other cells and is involved in a	2 73.0 cM	Cytokine	

V00755	1.00	-1.98	2.82	2.28	5.88	4.76	18.69	2.71	19.18	3.63	tissue inhibitor of metalloproteinase; Timp	V00755	metalloproteinase inhibitor 1 precursor (timp-1) (erythroid potentiating activity) (epa) (tissue inhibitor of metalloproteinases) (collagenase inhibitor 16c8 fibroblast) (tpa-induced protein) (tpa-s1).	complexes with metalloproteinases (such as collagenases) and irreversibly inactivates them. mediates erythropoiesis in vitro; but, unlike il-3, it is species -specific, stimulating growth and differentiation of only human and mouse cells.	X 6.2 cM	Proteolytic	
M19681	1.00	-1.30	6.02	2.91	3.70	2.69	36.38	2.49	18.47	6.24	small inducible cytokine A2; Scya2	M19681	small inducible cytokine a2 precursor (monocyte chemoattractant protein-1) (platelet-derived growth factor-inducible protein ie).	scya2 is expressed in activated mast cells, macrophages, and nerve cells...a b chemokine corresponding to the monocyte chemotactic protein, induced by pdgf. chemotactic factor that attracts monocytes and basophils, but not neutrophils or eosinophils. augments monocyte infiltrates, like psoriasis, rheumatoid arthritis, and atherosclerosis. may be involved in the recruitment of monocytes into the arterial wall during the disease process of atherosclerosis. binds	11 46.5 cM	Cytokine	
M60429	1.00	1.00	5.74	2.53	3.84	0.70	3.70	1.99	16.94	1.62	immunoglobulin heavy chain 4 (serum IgG1); Igh-4	M60429			12 58.0 cM		
Msa.34452.0	1.00	1.00	1.19	0.94	8.43	9.68	7.55	1.29	15.96	6.85	insulin-like growth factor binding protein 4; Igfbp4	AA117813	insulin-like growth factor binding protein 4 precursor (igfbp-4) (igfbp-binding protein 4).	igf-binding proteins prolong the half-life of the igfs and have been shown to either inhibit or stimulate the growth promoting effects of the igfs on cell culture. they alter the interaction of igfs with their cell surface receptors.		Extracellular Protein	

Table 1. Properties of cathelin-like proteins

Accession	1.00	4.36	6.28	1.96	3.34	0.80	3.60	1.19	14.16	0.37	cathelin-like protein; Cnlp	X94353	cathelin-related antimicrobial peptide precursor (cramp) (cathelin-like protein) (clp)	acts as a potent antimicrobial peptide.	961.0 cM	Metabolic
Msa.38664.0	1.00	1.00	3.40	0.91	2.76	1.76	5.71	1.59	13.90	3.18		AA144469				EST; Unknown
W49204	1.00	1.24	7.53	2.19	6.24	4.95	7.85	4.84	13.67	4.24	glypican 1; Gpc1	W49204				
X66473	1.00	1.79	0.70	1.41	2.92	4.00	10.73	1.24	13.46	1.70	matrix metalloproteinase 13; Mmp13	X66473	collagenase 3 precursor (ec 3.4.24.1) (matrix metalloproteinase-13) (mmp-13).	degrades collagen type I. does not act on gelatin or casein. could have a role in tumoral process. regulator of matrix remodeling component of the mmp cluster, expressed in the synovial membrane and synovial fibroblasts.		Proteolytic
L37297	1.00	2.53	6.23	1.63	2.38	0.66	3.08	1.11	12.74	1.56	neutrophilic granule protein; Ngp	L37297		a novel myeloid-specific granule protein related to porcine cathelin, but showing important structural differences. this may represent the first isolated member of a new cystatin family. more importantly, the small size of the protein binds to p-, e- and l-selectins. the calcium-dependent high affinity interaction with p-selectin mediates the tethering and rolling of neutrophils and lymphocytes on endothelial cells.		Intracellular Protein
X91144	1.00	2.10	3.53	1.24	4.04	2.92	10.33	0.54	12.68	2.95	selectin, platelet (p-selectin) ligand; Selpl	X91144	p-selectin glycoprotein ligand 1 precursor (psgl-1) (selectin p ligand).	binds to p-, e- and l-selectins. the calcium-dependent high affinity interaction with p-selectin mediates the tethering and rolling of neutrophils and lymphocytes on endothelial cells.	564.0 cM	Extracellular Protein
X54542	1.00	1.37	2.99	1.71	1.36	0.24	8.15	2.35	12.39	3.14	interleukin 6; Il6	X54542	interleukin-6 precursor (il-6) (interleukin hp-1) (b cell hybridoma growth factor).	il6 may be the most extremely pleiotropic of cytokines, with a broad range of activities on different cell types.	517.0 cM	Cytokine

Table 1. Characteristics of the proteins

X81627	1.00	1.92	3.27	1.14	2.57	0.96	12.19	0.13	11.79	2.91	lipocalin 2; Lcn2	X81627	neutrophil gelatinase-associated lipocalin precursor (ngal) (p25) (sv-40) induced 24h3	capable of carrying small lipophilic molecules like retinol, steroids, and odorants.	2 27.0 cM	Extracellular Protein	*
ET62052	1.00	1.06	5.14	2.14	3.73	0.87	3.52	1.29	11.69	0.43	immunoglobulin heavy chain 4 (serum IgG1); IgH-4	ET62052			12 58.0 cM		
W44075	1.00	1.61	5.43	2.30	3.25	1.18	3.35	1.14	11.54	2.21	myeloperoxidase; Mpo	W44075	myeloperoxidase precursor (ec 1.11.1.7) (mpo).	this enzyme is present in primary granules of neutrophils and plays a major role in the oxygen-dependent microbicidal system of granulocytes	11 49.0 cM	Intracellular Protein	
Msa.6242.0	1.00	-1.69	-1.10	2.37	4.33	3.18	8.04	2.31	10.59	1.01	cathepsin K; Ctsk	W13263	cathepsin k precursor (ec 3.4.22.38).	closely involved in osteoclastic bone resorption and may participate partially in the disorder of bone remodeling. displays potent endoprotease activity against fibrinogen at acid ph. may play an important role in extracellular matrix degradation	3 47.9 cM	Proteolytic	*
U59488	1.00	1.09	2.63	0.99	2.49	0.01	12.29	1.48	9.98	2.50	neutrophil cytosolic factor 4; Ncf4	U59488	neutrophil cytosol factor 4 (ncf-4) (neutrophil nadph oxidase factor 4) (p40-phox) (p40phox).	nadph oxidase consists of proteins p47-phox, p67-phox, p4-phox, and a small regulatory g protein. p4-phox is not required for oxidase activity and has been proposed to have a regulatory function	15 47.2 cM	Intracellular Protein	
Z12297	1.00	-1.13	2.36	1.52	2.47	4.30	14.05	0.57	9.42	1.82	small inducible cytokine A7; Scya7	Z12297	small inducible cytokine a7 precursor (monocyte chemotactic protein 3) (mcp-3) (monocyte chemoattractant protein 3) (intercrine/chemokine)	chemotactic factor that attracts monocytes and eosinophils, but not neutrophils. augments monocyte anti-tumor activity (by similarity). also induces release of gelatinase b. binds to ccr1, ccr2, ccr3.	11 46.5 cM	Cytokine	*

Table 1. Amino acid sequence of the protein and its properties.

C76739	1.00	1.00	1.85	1.03	2.46	3.48	12.67	2.14	9.30	2.34	macrophage C-type lectin; Mpcl	C76739			a type ii transmembrane protein with a single extracellular c-type lectin domain. expressed in cell lines and normal mouse tissues in a macrophage-restricted manner.	6 56.5 cM	Cell Surface Protein		*
U60438	1.00	1.09	2.36	0.99	2.45	1.31	17.95	6.58	8.54	2.10	serum amyloid A 2; Saa2	U60438	serum amyloid a-2 protein precursor [contains: amyloid protein a (amyloid fibril protein aa)].		saa1, saa2, and saa3 encode acute phase response proteins in response to inflammatory stimuli. acts as a precursor of the amyloid a protein that is a major constituent of amyloid fibrils formed in secondary amyloidosis.	7 23.5 cM	Other		*
X94444	1.00	-1.35	-0.12	1.31	3.13	2.06	5.71	1.36	8.43	0.90	cathepsin K; Cisk	X94444	cathepsin k precursor (ec 3.4.22.38).		cathepsin k (ec 3.4.22.38), encoded in the mouse by cisk, is implicated in bone resorption. expression is predominantly in osteoclasts; embryonic expression also takes place in some hypertrophic chondrocytes of growth cartilage.	3 47.9 cM	Proteolytic		*
M73748	1.00	-1.54	1.94	0.96	2.06	0.54	9.36	1.95	8.21	1.69	glycoprotein 38; Gp38	M73748	glycoprotein 38 precursor (gp38) (ots-8).				Cell Surface Protein		*
X83601	1.00	1.04	0.95	1.04	1.89	3.72	14.68	1.06	8.18	2.71	pentaxin related gene; Ptx3	X83601	pentaxin-related protein ptx3 precursor (tumor necrosis factor-inducible protein tsg14).		a tnfr stimulated gene. produced outside of the liver, increased levels of expression are induced by lps.	3 33.8 cM	Extracellular Protein		*
X96639	1.00	-1.20	1.41	0.88	1.95	0.27	4.72	1.16	8.11	2.12	exostosin (multiple) 1; Extl1	X96639	exostosin-l (putative tumor suppressor protein extl1) (multiple exostosin protein 1).		appears to be a tumor suppressor.	15 26.55 cM	Other		*

Table 1. Properties of the proteins

Msa.739.0	1.00	-1.82	-1.01	2.43	0.89	2.70	6.58	0.93	6.75	0.72	haptoglobin; Hp	M96827		haptoglobin combines with free plasma hemoglobin, preventing loss of iron through the kidneys and protecting the kidneys from damage by hemoglobin, while making the hemoglobin accessible to degradation	8 55.0 cM	Extracellular Protein	
D37837	1.00	1.26	1.48	0.88	2.18	0.80	5.85	1.31	6.34	1.47	plastin 2, L; Pls2	D37837	I-plastin (lymphocyte cytosolic protein 1) (lcp-1) (65 kDa macrophage protein) (m65)	actin-bundling protein.		Structural Protein	
U17961	1.00	1.15	4.42	0.90	3.16	1.65	7.12	1.45	6.33	1.79	src associated in mitosis, 68 kDa; Sam68	U17961					
U83903	1.00	-1.40	0.77	1.17	1.33	3.57	8.40	3.12	6.29	0.55	tumor necrosis factor induced protein 6; Tnfrp6	U83903		induced in vitro in several cell types by proinflammatory cytokines, and in vivo in pathological conditions such as rheumatoid arthritis. interacts with link protein and aggrecan. involved in matrix dissociation and regulated by ph	2	Regulatory	
M59378	1.00	1.72	2.24	0.60	2.28	1.03	7.57	0.87	6.26	1.20	tumor necrosis factor receptor superfamily, member 1b; Tnfrsf1b	M59378	tumor necrosis factor receptor 2 precursor (tnfr2) (p75).	encodes the larger of two receptors for the tumor necrosis factor. its expression is regulated by external factors. a tnfrsf1b targeted null mutation shows normal t-cell development and activity, but is resistant to tnfr-induced cell death.	4 75.5 cM	Receptor	

U16985	1.00	1.02	1.86	0.93	1.83	0.19	5.30	0.24	6.23	1.04	lymphotoxin B; Ltb	U16985	lymphotoxin-beta (tumor necrosis factor c).	member of the tnfr ligand family isolated from human t cells. only found on the cell surface, where it forms a 2:1 trimeric complex with lymphotoxin a. constitutively expressed in lymphoid and hematopoietic tissues, maximal in thymic medulla and splenic white pulp may play a specific role in immune response regulation. provides the membrane anchor for the attachment of the	17 19.06 cM	Cytokine		*
Msa.1700.0	1.00	2.40	-0.32	0.82	2.12	3.77	5.59	2.04	5.93	0.88	phospholipase A2 group VII (platelet-activating factor acetylhydrolase, plasma); Pla2g7	U34277	platelet-activating factor acetylhydrolase precursor (ec 3.1.1.47) (paf acetylhydrolase) (paf 2-acylhydrolase) (ldl-associated phospholipase a2) (ldl-pla(2)) (2-acetyl-1-alkylglycerophosphocholine esterase) (1-alkyl-2-acetyl-glycerophosph	modulates the action of platelet-activating factor (paf) by hydrolyzing the sn-2 ester bond to yield the biologically inactive lyso-paf. has a specificity for substrates with a short residue at the sn-2 position. it is inactive against lo		Cytokine		
AA059883	1.00	-1.03	0.28	1.16	3.05	4.37	8.59	2.30	5.91	0.99	angiopoietin related	AA059883		the region of this genomic sequence that contains this sequence is listed as angiopoietin related.		Hemostasis		*

Table 1. Properties of the genes identified in the library.

Accession	1.00	-1.30	0.82	0.94	3.68	2.47	5.23	1.66	5.79	1.04	hexosaminidase A; Hexa	U05837	beta-hexosaminidase alpha chain precursor (ec 3.2.1.52) (n-acetyl-beta-glucosaminidase) (beta-n-acetylhexosaminidase) (hexosaminidase a).	lysosomal enzymes that contribute to the degradation of glycoproteins, glycolipids, and glycosaminoglycans. widely expressed, associated with ganglioside degradation. absence of the b form is associated with Tay-Sachs disease.	9 29.0 cM	Protoclytic	
Msa.1600.0	1.00	1.12	-0.54	1.14	0.56	2.11	4.88	0.13	5.61	0.65	macrophage expressed gene 1; Mpeg1	L20315		transcripts from the gene are found at a high level in mature human and murine macrophages and at a moderate level in certain myelomonocytic cell lines		EST; Unknown	
L32974	1.00	-2.05	1.79	0.94	0.01	1.10	1.71	0.31	5.57	1.47	interferon-induced protein with tetratricopeptide repeats 3; Ifit3	L32974	interferon-induced protein with tetratricopeptide repeats 3 (ifit-3) (glucocorticoid-attenuated response gene 49 protein) (gras-49) (ira2)				
AA387033	1.00	1.17	1.46	0.66	2.73	1.63	5.21	0.80	5.54	0.46	Unknown	AA387033				EST; Unknown	
U72643	1.00	1.61	0.59	0.80	0.84	2.13	5.65	0.13	5.50	0.94	leucocyte specific transcript 1; Lst1	U72643		defense/immunity protein. an integral membrane protein.	17 19.06 cM	EST; Unknown	
AA174982	1.00	-1.02	1.24	0.85	3.75	2.69	5.03	1.76	5.39	0.63	coronin, actin binding protein 1A; Corola	AA174982	coronin-like protein p57 (coronin 1a) (fragment).	coronin participates in the remodelling of the cortical actin cytoskeleton that is responsible for phagocytosis and macropinocytosis. in mammalian neutrophils, a coronin-like protein is also associated with the cytoskeleton.	7 62.5 cM	Intracellular Protein	

Table 1. Summary of the data obtained from the analysis of the expression of the genes in the different cell lines.

Msa.2530.0	1.00	1.00	1.30	0.30	1.23	0.23	5.83	1.26	4.66	1.14	vav oncogene; Vav	X64361	vav proto-oncogene.	probable exchange factor for a small ras-like gtp-binding protein. can be activated by truncation of the n-terminus.	17 32.7 cM	Signal Transduction	
X07640	1.00	-1.80	1.45	0.57	0.02	1.79	4.71	1.02	4.65	0.90	integrin alpha M (Cd11b); Itgam	X07640	cell surface glycoprotein mac-1 alpha subunit precursor (cr-3 alpha chain) (cd11b) (leukocyte adhesion receptor molecule) (integrin alpha m).	mac-1 is a cell surface glycoprotein of monocytes, macrophages and granulocytes which has been implicated in various adhesive interactions of these cells as well as in mediating the uptake of complement-coated particles. mac-1 is identical with cr-3, the receptor for the ic3b fragment of the third complement component. mac-1 probably recognize the		Cell Surface Protein	
Msa.641.0	1.00	-1.03	-0.19	1.41	1.05	2.42	4.35	0.06	4.63	0.84	Fc receptor, IgE, high affinity 1, gamma polypeptide; Fcrlg	W41745	high affinity immunoglobulin epsilon receptor gamma-subunit precursor (fcrlg) (ige fc receptor, gamma-subunit) (fc-epsilon-ri-gamma)	the gamma subunit has a critical role in allowing the ige fc receptor to reach the cell surface	193.3 cM	Receptor	
D10911	1.00	-1.22	1.65	0.35	2.18	1.00	4.95	0.08	4.59	0.99	a disintegrin and metalloprotease domain (ADAM) 8; Adam8	D10911	adam 8 precursor (ec 3.4.24.-) (a disintegrin and metalloproteinase domain 8) (cell surface antigen ms2) (macrophage cysteine-rich glycoprotein) (cd156 antigen)	possible involvement in extravasation of leukocytes.	7 F3-F5	Proteolytic	
X15591	1.00	1.53	0.39	0.89	0.63	1.86	3.57	0.27	4.58	0.64	cytotoxic T lymphocyte-associated protein 2 alpha: Cita2a	X15591	ctla-2-alpha protein precursor.	not known, expressed in activated t-cell.	13 36.0 cM	Cell Surface Protein	

Cell Surface Protein

AA285691	1.00	1.21	0.98	0.77	2.15	3.40	6.67	2.62	4.57	0.72	cytohesin binding protein (Cbp)	AA285691		bone marrow-derived dendritic cells"" ""cloned by subtraction of activated bone marrow macrophage versus bone marrow-derived dendritic cells""		Cell Surface Protein	
Msa.1529.0	1.00	1.00	0.58	0.47	0.44	0.64	2.46	0.31	4.50	0.60	growth factor receptor bound protein 10; Grb10	U18996	growth factor receptor-bound protein 10 (grb10 adaptor protein).	plays a functional role in insulin and igf-i signaling. may serve to positively link the insulin and igf-i receptors to an uncharacterized mitogenic signaling pathway. interacts with the cytoplasmic domain of the autophosphorylated insulin receptor which is then inhibited. the interaction is mediated by the sh2 domain. also binds activated platelet-derived growth factor receptor and epidermal growth	11 8.0 cM	Signal Transduction	
X67783	1.00	2.51	0.70	0.76	0.80	1.94	2.37	0.17	4.49	0.49	vascular cell adhesion molecule 1; Vcam1	X67783	vascular cell adhesion protein 1 precursor (v-cam 1).	cell-cell recognition. appears to function in leukocyte-endothelial cell adhesion. interacts with beta-1 integrin vla4 on leukocytes, and mediates both adhesion and signal transduction. vcam1/vla4 interaction may play a pathophysiologic role	3 50.8 cM	Cell Surface Protein	
X81582	1.00	-1.60	-0.48	1.27	0.82	2.27	2.74	0.12	4.48	0.38	insulin-like growth factor binding protein 4; Igfbp4	X81582	insulin-like growth factor binding protein 4 precursor (igfbp-4) (ibp-4) (igf binding protein 4).	binding proteins may act to distribute the igfs among the body fluid compartments, to protect the body from possible hypoglycemic effects of the igfs		Extracellular Protein	

*

Msa.2034.0	1.00	-1.02	0.25	0.81	1.38	2.45	5.16	0.29	4.46	0.72	CD53 antigen; Cd53	X97227	leukocyte surface antigen cd53 (cell surface glycoprotein cd53).	may be involved in growth regulation in hematopoietic cells.	3 50.5 cM	Cell Surface Protein	
AA103744	1.00	-1.31	1.73	1.20	3.98	2.12	7.13	2.86	4.42	0.81	ribosomal protein L27a; Rpl27a	AA103744	60s ribosomal protein 127a (129).	plays cardinal role in calcium metabolism, and may be involved in neural transmission. buffers cytosolic calcium. may stimulate a membrane ca(2+)-atpase and a 3',5'-cyclic nucleotide phosphodiesterase. expressed in many	7 E2-F1	Metabolic	
AA189487	1.00	1.16	0.09	0.68	1.28	2.89	4.40	1.72	4.39	0.91	sushi-repeat-containing protein, X chromosome; SrpX-pending	AA189487				EST; Unknown	
Msa.1843.0	1.00	-1.25	0.33	0.73	0.53	1.90	5.85	0.19	4.32	1.17	chemokine (C-C) receptor 1, chemokine (C-C) receptor 1-like 2; Cmkbr1, Cmkbr112	U28404	c-c chemokine receptor type 1 (c-c ckr-1) (cc-ckr-1) (ccr-1) (ccr1) (macrophage inflammatory protein-1 alpha receptor) (mip-1 alpha-r) (rantes-r)., probable c-c chemokine receptor type 3 (c-c ckr-3) (cc-ckr-3) (ccr-3) (ccr3) (macrophage inflammatory protein-1 alpha receptor-like 2)	mip-1a-receptor. all three of the cmkbr1 genes has been found in leukocytes, but their patterns of expression differ in solid organs. cmkbr1 is expressed in heart, spleen, and lung;	9 72.0 cM	Receptor	
Msa.31660.0	1.00	-1.04	0.86	0.72	0.81	2.03	4.38	0.48	4.28	0.73	CD53 antigen; Cd53	AA105582	leukocyte surface antigen cd53 (cell surface glycoprotein cd53).	may be involved in growth regulation in hematopoietic cells.	3 50.5 cM	Cell Surface Protein	
U29947	1.00	-1.41	-2.19	1.91	3.44	5.25	7.01	4.87	4.27	1.44	mannosidase 2, alpha B1; Man2b1	U29947	lysosomal alpha-mannosidase precursor (ec 3.2.1.24) (mannosidase, alpha b) (lysosomal acid alpha-mannosidase) (laman)	necessary for the catabolism of n-linked carbohydrates released during glycoprotein turnover. cleaves all known types of alpha-mannosidic linkages.	8 37.0 cM	Regulatory	

Accession number	1.00	-2.14	0.74	0.79	2.40	1.24	3.20	0.63	4.20	0.32	myristoylated alanine-rich C kinase substrate; Macs	AA546670	myristoylated alanine-rich C-kinase substrate (marcks).	10 22.0 cM	marcks is the most prominent cellular substrate for protein kinase c. this protein binds calmodulin, actin, and synapsin. marcks is a filamentous (f) actin cross-linking protein.	
AA546670	1.00	-2.14	0.74	0.79	2.40	1.24	3.20	0.63	4.20	0.32	myristoylated alanine-rich C kinase substrate; Macs	AA546670	myristoylated alanine-rich C-kinase substrate (marcks).	10 22.0 cM	marcks is the most prominent cellular substrate for protein kinase c. this protein binds calmodulin, actin, and synapsin. marcks is a filamentous (f) actin cross-linking protein.	
Msa.40979.0	1.00	-1.35	2.97	0.90	1.29	2.51	3.55	1.17	4.19	1.07		AA161769				
AA544540	1.00	-1.10	2.67	0.86	2.10	1.04	4.47	1.05	4.18	0.85		AA544540				
Msa.1099.0	1.00	1.13	0.92	0.61	2.24	0.74	3.25	0.27	4.15	0.40	neuron specific gene family member 1; Nsg1	W46015	neuron specific protein family member 1 (brain neuron cytoplasmic protein 1) (p21) (m234)	5 21.0 cM	EST; Unknown	
U36993	1.00	1.03	0.47	0.64	0.33	1.42	4.96	1.07	4.12	0.97	cytochrome P450, 7b1; Cyp7b1	U36993	cytochrome p450 7b1 (oxysterol 7-alpha-hydroxylase) (ec 1.14.13.-) (hct-1).	3 1.0 cM	heme-containing enzymes involved in metabolism of a number of endogenous substrates. expressed principally in brain, only low levels found in liver. most closely resembles p45vii1, cholesterol 7 a hydroxylase, but classed differently from it.	Metabolic
AA170444	1.00	1.16	1.10	0.52	1.15	0.07	2.61	0.32	4.04	0.68	EST; Unknown	AA170444			EST; Unknown	
AA289661	1.00	-1.32	0.82	0.90	1.52	2.69	4.34	0.86	4.01	0.60	EST; Unknown	AA289661			EST; Unknown	
K01496	1.00	-1.66	0.56	0.76	1.77	3.25	4.14	1.13	4.01	0.40	histocompatibility 2, complement component B; H2-Bf	K01496	complement factor b precursor (ec 3.4.21.47) (c3/c5 convertase).	17 18.85 cM	factor b which is part of the alternate pathway of the complement system is cleaved by factor d into 2 fragments: ba and bb. ba, a serine protease, then combines with complement factor 3b to generate the c3 or c5 convertase.	Hemostasis

AA189758	1.00	-1.21	1.44	0.52	2.27	1.23	5.25	0.42	4.00	0.32	Wbscr5 gene product; Wbscr5	AA189758	(see note) contains two lim domains and a putative protein kinase domain. high expression levels in CNS, particularly in spinal cord, cranial nerve and dorsal root ganglia. lesser expression in heart and skeletal muscle. may be a component of	Regulatory	
U88328	1.00	1.73	0.18	0.87	1.95	4.32	5.37	1.50	4.00	0.28	cytokine inducible SH2-containing protein 3 (SOCS3); Cish3	U88328	cytokine inducible SH2-containing protein 3 (protein effector 10).	ECM (Matrix Prot)	
AA015322	1.00	1.70	-1.39	0.77	-0.73	2.09	2.86	2.87	3.98	1.02	SPARC-related protein (SRG) (related to osteonectin)	AA015322		Other	
M13963	1.00	-1.39	2.19	0.75	1.70	0.25	3.64	1.35	3.92	0.80	guanine nucleotide binding protein, alpha inhibiting 2; Gnai2	M13963	guanine nucleotide-binding protein g(i), alpha-2 subunit (adenylate cyclase-inhibiting g alpha protein).	Signal Transduction	9 59.0 cM
Z16078	1.00	1.06	0.06	1.04	0.83	2.18	3.64	0.16	3.92	0.55	CD53 antigen; Cd53	Z16078	leukocyte surface antigen cd53 (cell surface glycoprotein cd53).	Cell Surface Protein	3 50.5 cM
M63836	1.00	-1.50	-0.08	0.81	0.65	2.02	3.88	0.75	3.87	0.12	beta-glucuronidase structural; Gus-s	M63836	beta-glucuronidase precursor (ec 3.2.1.31).	Metabolic	5 72.0 cM
D11468	1.00	1.82	1.20	0.78	2.26	0.93	0.95	1.00	3.84	1.15	immunoglobulin alpha heavy chain	D11468		Extracellular Protein	
AA266385	1.00	-1.03	1.00	0.58	1.12	0.04	3.88	0.46	3.84	0.84	DNA segment, Chr X, Immunex 39, expressed;	AA266385		EST; Unknown	X 1.6 cM

U29762	1.00	3.11	2.20	1.45	5.23	2.30	3.07	1.90	3.83	1.07	D site albumin promoter binding protein; Dbp	U29762	d-site-binding protein (albumin d box-binding protein).	this transcriptional activator recognizes and binds to the sequence 5'-rttagtaay-3' found in the promoter of genes such as albumin, cyp2a4 and cyp2a5. it is not essential for circadian rhythm generation, but modulates important clock output genes. may be a direct target for regulation by the circadian pacemaker component clock. may affect circadian period	7 23.0 cM	Transcription Factor
AA177433	1.00	1.34	0.21	0.82	0.49	2.05	4.56	0.86	3.82	0.51	EST; Unknown	AA177433				EST; Unknown
D28599	1.00	-1.28	0.91	0.59	1.18	0.13	4.59	0.54	3.81	0.96	chondroitin sulfate proteoglycan 2; Cspg2	D28599	versican core protein precursor (large fibroblast proteoglycan) (chondroitin sulfate proteoglycan core protein 2) (nc-m)	extracellular matrix link protein.	13 55.0 cM	ECM (Matrix Prot)
D50494	1.00	-2.14	11.79	6.74	3.21	2.21	4.11	1.50	3.78	0.92	DEAD (aspartate-glutamate-alanine-aspartate) box polypeptide 6; Ddx6	D50494	probable ATP-dependent RNA helicase p54 (oncogene rck homolog) (dead-box protein 6)		9 26.0 cM	
L15443	1.00	1.18	0.10	1.49	2.42	0.90	3.03	0.39	3.78	0.42	membrane component, surface marker 1; M3sl	L15443				Cell Surface Protein
ET62103	1.00	-1.46	10.80	4.19	6.12	8.71	6.88	5.42	3.78	2.72	apoptosis inhibitor 1; birc2 (Apl1)	ET62103	inhibitor of apoptosis protein 1 (miap1) (miap-1).	traf1 and/or traf2 associated protein of the iap (inhibitor of apoptosis) family. iaps may play a role in tumour progression rather than tumour initiation, making the iaps an attractive therapeutic target	9 A2	Regulatory
U88908	1.00	1.55	1.04	0.58	1.90	0.66	5.13	1.33	3.77	0.55		U88908				

AA020512	1.00	1.01	1.31	0.45	1.33	0.02	3.97	0.39	3.75	0.87	caspase 6; Casp6	AA020512	caspase-6 precursor (ec 3.4.22.-) (apoptotic protease mch-2).	involved in the activation cascade of caspases responsible for apoptosis execution. cleaves poly(adp-ribose) polymerase in vitro, as well as lamins. overexpression promotes programmed cell death (by apoptosis).			*
AA172851	1.00	-1.04	0.26	0.77	0.44	1.66	4.53	0.34	3.75	0.58	EST; Unknown	AA172851		no match on blast	EST; Unknown		
X75926	1.00	2.26	0.55	0.56	1.93	0.81	2.51	0.07	3.74	0.54	ATP-binding cassette, sub-family A (ABC1), member 1; Abca1	X75926	atp-binding cassette, sub-family a, member 1 (atp-binding cassette transporter 1) (atp-binding cassette 1) (abc-1)	camp-dependent and sulfonyleurea-sensitive anion transporter. key gatekeeper influencing intracellular cholesterol transport (by similarity)	4 23.1 cM		
Msa.22134.0	1.00	-1.17	-0.52	1.02	2.09	0.87	3.68	0.40	3.72	0.48	Unknown	AA031158			EST; Unknown		
U59463	1.00	1.12	1.47	0.50	1.56	0.11	3.86	0.75	3.72	0.86	caspase 11; Casp11	U59463	caspase-11 precursor (ec 3.4.22.-) (ich-3 protease).	involved in the activation cascade of caspases responsible for apoptosis execution. promotes interleukin-1 beta processing by ice, so may also have a role in inflammatory responses			*
Msa.510.0	1.00	-2.49	-0.90	1.04	0.25	1.81	2.97	0.16	3.71	0.50	histocompatibility 2, complement component factor B; H2-Bf	M57890	complement factor b precursor (ec 3.4.21.47) (c3/c5 convertase).	involved in the alternative or properdin complement pathway	17 18.85 cM	Hemostasis	
AA172673	1.00	1.32	1.17	0.44	1.53	0.29	3.48	0.41	3.70	0.63	paternally expressed gene 3; Peg3	AA172673			EST; Unknown		
AA051505	1.00	-2.70	-1.31	0.66	0.87	2.64	3.03	0.83	3.70	0.72	EST; unknown	AA051505			EST; Unknown		
U89269	1.00	-1.43	0.80	0.75	2.05	3.22	4.88	1.64	3.69	0.60	cathepsin C; Ctsc	U89269	dipeptidyl-peptidase i precursor (ec 3.4.14.1) (dpp-i) (dppi) (cathepsin c) (cathepsin j) (dipeptidyl transferase).	mammalian lysosomal cysteine proteinases. plays a role in protein catabolism within the cell, and may be involved in tumor metastasis. expression is widely distributed, with some variability in level, in mouse tissues	7 D3-E1.1	Proteolytic	*

J03535	1.00	-1.00	0.79	0.72	2.43	1.30	3.93	1.01	3.68	0.20	embigin; Emb	J03535	pou domain, class 6, transcription factor 1 (octamer-binding transcription factor emb) (transcription regulatory protein mep-1), teratocarcinoma glycoprotein gp-70 precursor.	embigin and basigin are highly glycosylated transmembrane glycoproteins with two immunoglobulin domains and form a subgroup in the immunoglobulin superfamily. embigin is strongly expressed in the endoderm	15 57.0 cM	Transcription Factor	
AA592768	1.00	1.54	2.46	0.83	4.64	1.76	5.53	2.15	3.66	0.49	small proline-rich protein 2A; Spr2a	AA592768		small proline-rich (spr) proteins are structural components of the cornified cell envelope of stratified squamous epithelia, they are subdivided into three families, i.e., spr1, spr2, and spr3, of which the spr2 family is the most	3 45.2 cM	Structural Protein	
AA259937	1.00	-5.79	-1.14	0.85	0.60	2.69	2.67	0.61	3.65	0.51	procollagen, type III, alpha 1; Col3a1	AA259937	collagen alpha 1(iii) chain precursor.	collagen type iii occurs in most soft connective tissues along with type i	1 21.1 cM	ECM (Matrix Prot)	*
M31419	1.00	1.09	1.63	0.64	1.42	0.20	4.04	0.65	3.65	1.09	interferon activated gene 204; Ifi204	M31419	interferon-activatable protein 204 (ifi-204) (interferon-inducible protein	member of a cluster of genes activated by interferon on chr 1. function unknown.	1 95.2 cM	Unknown	*
X13333	1.00	-1.22	-0.21	0.70	0.54	1.83	3.09	0.31	3.65	0.66	CD14 antigen; Cd14	X13333	monocyte differentiation antigen cd14 precursor (lps receptor) (lps-r) (myeloid cell-specific leucine-rich glycoprotein).	a cell surface marker of human monocytes and macrophages. serves as an lps receptor controlling cell activation under physiological conditions. when lps binds to cd14 the cells become activated and release cytokines and	18 31.0 cM	Cell Surface Protein	*
Msa.17760.0	1.00	1.18	-0.09	0.59	1.30	0.26	2.25	0.17	3.65	0.46		W98059					
Msa.10687.0	1.00	-7.85	-1.32	1.27	0.53	1.55	2.43	0.50	3.62	0.29	Unknown	W48936				EST; Unknown	

Cell Adhesion

D16262	1.00	-2.89	-2.10	0.78	-0.63	1.88	1.84	0.27	3.59	0.99	mesoderm specific transcript; Mest	D16262		aka peg-1 -- the mouse peg1/mest gene is an imprinted gene that is expressed particularly in mesodermal tissues in early embryonic stages	6 7.5 cM	Cytokine	
M31131	1.00	-1.13	0.01	0.80	0.44	1.57	2.15	0.39	3.58	0.51	cadherin 2; Cdh2	M31131	neural-cadherin precursor (n-cadherin).	cadherins are calcium dependent cell adhesion proteins. they preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types. n-cadherin may be involved in	18 6.0 cM	Cell Surface Protein	
AA161790	1.00	-1.89	2.16	0.67	2.68	0.16	3.54	0.34	3.56	0.25	aplysia ras-related homolog A2; Arha2	AA161790		regulates a signal transduction pathway linking plasma membrane receptors to the assembly of focal adhesions and actin stress fibers	2 37.0 cM	Intracellular Protein	
D83266	1.00	-1.47	0.12	0.69	0.47	1.66	4.05	0.84	3.55	0.78	vav oncogene; Vav	D83266	vav proto-oncogene.	binds to grb2 and grb3	17 32.7 cM	Signal Transduction	*
M35833	1.00	-1.98	-1.06	0.88	0.24	1.52	0.75	0.95	3.54	0.48	midkine; Mdk	M35833	midkine precursor (retinoic acid-induced differentiation factor).	midkine (mk) is a heparin-binding growth/differentiation factor implicated in the control of development and repair of various tissues. mk plays important roles in chondrogenesis and contributes to bone	2 53.0 cM	Cytokine	*

L23801	1.00	-1.89	-2.21	1.27	0.70	2.36	2.59	0.70	3.54	0.51	integrin binding sialoprotein; Ibsp	L23801	bone sialoprotein ii precursor (bsp ii) (cell-binding sialoprotein) (integrin-binding sialoprotein).	aka integrin binding sialoprotein -- bone sialoprotein (bsp) is a small, highly posttranslationally modified integrin binding protein found in the mineral compartment of developing bone. contains a conserved arg-gly-asn (rgd) sequence.	556.0 cM	ECM (Matrix Prot)	
U78818	1.00	-2.25	1.14	0.45	1.09	0.02	3.63	0.37	3.54	0.45	downstream of tyrosine kinase 1; Dok1	U78818			634.73 cM		
U19482	1.00	-1.31	1.07	0.85	1.65	2.68	6.02	0.87	3.52	0.32	small inducible cytokine A9; Scya9	U19482	small inducible cytokine a9 precursor (macrophage inflammatory protein 1-gamma) (mip-1-gamma) (macrophage inflammatory protein-2) (mrp-2) (ccf18).	a.k.a mip-1 gamma or ccf18 -- chemokines play an important role in immune and inflammatory responses by inducing migration and adhesion of leukocytes. ccf18 mma is constitutively expressed in macrophage and endothelial cells.	1147.4 cM	Cytokine	*
U21795	1.00	-1.16	1.05	0.42	1.53	0.36	4.01	0.56	3.51	0.61	interleukin 2 receptor, gamma chain; IL2rg	U21795	cytokine receptor common gamma chain precursor (gamma-c) (interleukin-2 receptor gamma chain) (il-2r gamma chain) (n664)	common subunit for the receptors for a variety of interleukins.	X38.0 cM		*
M27960	1.00	-1.14	-0.88	1.09	1.29	2.91	5.45	0.51	3.49	0.49	interleukin 4 receptor, alpha; IL4ra	M27960	interleukin-4 receptor alpha chain precursor (il-4r- alpha).	a receptor for il4, a mediator of the th2 (b cell) response. acts as an antagonist to il4, presumably by adsorbing il4 molecules.	762.0 cM	Receptor	*
W11156	1.00	0.01	0.61	1.10	1.64	0.10	3.19	0.05	3.49	0.67	EST; unknown	W11156		some similarity to j399 human gamma- interferon-inducible protein		EST; Unknown	

AA189512	1.00	-1.76	0.59	0.90	0.09	1.32	2.95	0.73	3.40	0.81	lymphocyte antigen 86; Ly86	AA189512						
L07063	1.00	-2.99	-1.77	1.08	-0.05	1.46	2.71	0.25	3.39	0.45	FK506 binding protein 6 (65 kDa); Fkbp6	L07063	65 kda f506-binding protein precursor (ec 5.2.1.8) (fkbp65) (fkbprp) (peptidyl-prolyl cis-trans isomerase) (ppiasc) (rotamase) (immunophilin fkbp65).	aka fkbp65 -- fkbp65 is a member of the f56-binding protein class of immunophilins and is the only member reported to contain four peptidylprolyl cis-trans isomerase domains and an unrelated cooh	11 58.0 cM	Intracellular Protein		
C79010	1.00	-1.16	0.57	0.74	0.20	1.36	2.95	0.16	3.38	0.63	Src-associated adaptor protein; Saps	C79010				??		
M16355	1.00	-8.28	0.30	1.12	0.93	2.07	2.65	0.61	3.38	1.03	major urinary protein 1; Mup1	M16355	major urinary protein 1 precursor (mup 1).	the mup proteins are lipocalins, and apparently take part in the transport of pheromones. though secreted in the urine, they are produced in the liver or in the lachrymal, mammary, and submaxillary glands	4 27.8 cM	Extracellular Protein		
C76049	1.00	1.55	1.84	0.21	1.84	0.32	5.59	0.86	3.38	0.87	EST; Unknown	C76049				EST; Unknown		
X80478	1.00	-1.17	-1.47	0.70	0.44	2.11	2.02	0.35	3.38	0.40	AE-binding protein 1; Aebp1	X80478		encodes a 845-aa protein that is almost identical to mouse adipocyte transcription factor aebp1. it is also expressed in a murine osteoblastic line, but is shut off in the final calcification phase, suggesting a transcriptional repressive eff		Transcription Factor		
M87276	1.00	1.13	2.06	0.24	2.43	0.87	2.49	0.07	3.34	0.37	thrombospondin 1; Thbs1	M87276	thrombospondin 1 precursor.	thrombospondin-1 functions as a cell adhesion molecule and also modulates cell movement, cell proliferation, neurite outgrowth and angiogenesis	2 65.0 cM	Extracellular Protein		

D87967	1.00	1.02	0.59	0.61	0.48	1.55	3.41	0.31	3.34	0.33	protein tyrosine phosphatase, non-receptor type substrate 1; Ptpn11	D87967			2 73.1 cM	Intracellular Protein	
AA617405	1.00	-1.26	1.56	0.56	1.50	0.41	4.69	0.77	3.32	0.66	EST; Unknown	AA617405				EST; Unknown	
AA230776	1.00	-1.20	0.86	0.52	1.28	2.33	2.78	0.57	3.29	0.37	thymosin beta 10 (prothymosin beta 10)	AA230776				beta-thymosins are a family of monomeric actin sequestering peptides that regulate actin dynamics within the cells. during embryogenesis the control of actin polymerization is essential in processes such as cell migration, cell division and so on.	
Msa.2614.0	1.00	-1.39	0.50	0.64	1.59	0.53	3.76	0.38	3.28	0.68	properdin factor, complement; Pfc	X12905	properdin (fragment).		X 6.2 cM	Extracellular Protein	
AF017989	1.00	-2.81	-2.56	1.30	0.09	2.39	1.91	0.42	3.28	0.60	stromal cell derived factor 5; Sdf5	AF017989			3 38.5 cM	Extracellular Protein	
M24509	1.00	1.04	2.36	0.66	2.25	0.67	3.25	0.83	3.27	0.73	ferritin heavy chain; Fth	M24509	ferritin heavy chain (ferritin h subunit).		19 2.0 cM		
Msa.4744.0	1.00	1.13	2.87	0.83	2.31	1.28	3.00	2.22	3.27	1.91	topoisomerase (DNA) I; Top1	W10047	dna topoisomerase I (ec 5.99.1.2).		2 92.0 cM		

U29539	1.00	-1.52	0.42	0.73	1.06	2.21	3.37	0.68	3.25	0.38	lysosomal-associated protein transmembrane 5; Laptm5	U29539	lysosomal-associated multitransmembrane protein (retinoic acid-inducible e3 protein).	the expression pattern of the gene together with preliminary evidence that the protein interacts with ubiquitin indicates that the protein may have a special functional role during embryogenesis and in adult hematopoietic cells. it			
AA125580	1.00	-1.07	1.43	0.44	1.46	0.06	3.65	0.56	3.22	0.64	synaptosomal-associated protein, 23kD; Shap23	AA125580			2 61.8 cM		
X93328	1.00	-1.75	0.32	0.79	0.38	1.69	3.03	0.17	3.21	0.44	EGF-like module containing, mucin-like, hormone receptor-like sequence 1; Emr1	X93328	cell surface glycoprotein emr1 precursor (emr1 hormone receptor) (cell surface glycoprotein f4/80)	probably involved in cell adhesion within tissues and receptor signalling.	17 34.3 cM	Cell Surface Protein	
Msa.35983.0	1.00	-1.10	-1.46	1.04	0.12	1.54	2.65	0.50	3.19	0.26	secreted phosphoprotein 1; Spp1	AA123395	precursor (bone sialoprotein 1) (minopontin) (early t lymphocyte activation 1 protein) (secreted phosphoprotein 1) (spp-1) (Zar) (calcium oxalate crystal growth inhibitor-neotoma)	binds tightly to hydroxyapatite. appears to form an integral part of the mineralized matrix. probably important to cell-matrix interaction.	5 56.0 cM	Cytokine	
Msa.2173.0	1.00	1.16	0.76	0.57	0.37	1.73	3.13	0.44	3.17	0.38	inhibin beta-A; Inhba	X69619	inhibin beta-a chain precursor (activin beta-a chain).	inhibin is a gonadal glycopeptide that inhibits the secretion of follicleotropin by the pituitary gland. on the other hand activin activates the secretion of follicleotropin. activin is also important in embryonic axial development.	13 10.0 cM	Cytokine	

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Table 1. Summary of protein data bank (PDB) entries for the human protein Lbp2.

Accession	Chain	Residues	Resolution (Å)	R-factor	Q-factor	B-factor (Å ²)	Temperature (K)	Source	Latent transforming growth factor beta binding protein 2; Lbp2	AF004874	Human protein is structurally similar to fibrillin. plays a role in bone biology? Itbp-2 gene expression in mouse embryos was restricted to cartilage perichondrium and blood vessels, a somewhat surprising result since other Itbp genes are expressed in all tissues, notably the	12 D	Unknown
AF004874													
L38971									integral membrane protein 2; Itm2	L38971	integral membrane protein 2a (c25 protein).	X 37.0 cM	
Msa.64.0									collagen binding protein 1; Cbp1	D12907	47 kda heat shock protein precursor (collagen-binding protein 1) (serine protease inhibitor i6).		Intracellular Protein
M31418									interferon activated gene 202A,interferon activated gene 202B; Ifi202a,Ifi202b	M31418	interferon-activatable protein 202a (ifi-202a) (interferon-inducible protein p202a),interferon-activatable protein 202b (ifi-202b) (interferon-inducible protein p202b).	1,1 95.2 cM	
AA177300									DNA segment, Chr 13, Abbott 1 expressed; D13Abb1e	AA177300	seven transmembrane domain protein, upregulated during kidney development.	13 6.0 cM	Cell Surface Protein
X56304									tenascin C; Tnc	X56304	extracellular matrix glycoprotein expressed in developing brain, mesenchyme, and cartilage, osteoblasts, periosteal and perichondrial cells, and articular surfaces, and is maintained into adult stages in some tissues, notably the	4 32.2 cM	ECM (Matrix Prot)

Table 1. Summary of the properties of the mouse monoclonal antibodies used in this study.

U05265	1.00	-1.14	0.38	0.61	0.20	1.56	4.01	0.57	3.06	0.66	glycoprotein 49 B; Gp49b	U05265	mast cell surface glycoprotein gp49a precursor, mast cell surface glycoprotein gp49b precursor.	preferentially expressed on mouse interleukin-3-dependent, bone marrow-derived mast cells, which are immature progenitor cells. members of the protein family are alternative splices of gp49a and gp49b.	10 32.0 cM	Cell Surface Protein	
D12907	1.00	-1.56	0.04	0.74	0.80	1.99	2.84	0.37	3.03	0.15	collagen binding protein 1; Cbp1	D12907	47 kda heat shock protein precursor (collagen-binding protein 1) (serine protease inhibitor ig)	binds specifically to collagen. could be involved as a chaperone in the biosynthetic pathway of collagen.		Intracellular Protein	
D86422	1.00	7.64	1.04	1.06	7.03	8.15	0.24	1.30	3.03	1.86	keratin-associated protein 8-2; Krtap8-2	D86422					
V00802	1.00	3.13	1.02	0.89	2.20	0.79	0.74	0.96	3.02	0.42		V00802				EST; Unknown	
AA408463	1.00	1.15	-0.68	0.55	0.66	2.06	2.37	0.79	3.02	0.25	probable match to cadherin 5	AA408463		vasculo-endothelial (ve)-cadherin is specifically expressed in endothelial cells. expressed in ubiquitously in vascular structures. cadherins act as cell adhesion receptors.		Cell Surface Protein	
U52524	1.00	-1.35	0.32	0.62	0.41	1.81	3.16	0.79	3.00	0.56	hyaluronan synthase 2; Has2	U52524	hyaluronan synthase 2 (ec 2.4.1.-) (hyaluronate synthase 2) (hyaluronic acid synthase 2) (ha synthase 2)	play a role in hyaluronan/hyaluronic acid (ha) synthesis.	15 31.2 cM	Other	
X14951	1.00	-1.02	0.33	0.69	0.52	2.07	2.90	0.25	2.99	0.46	integrin beta 2 (Cd18); Itgb2	X14951	cell surface adhesion glycoproteins lfa-1/cr3/p150,95 beta-subunit precursor (integrin beta-2) (cd18 antigen) (complement receptor c3 beta-2)	associates with alpha-l (lfa-1) to interact with icam-1, and with alpha-x m (mac-1) or alpha-x to form the receptor for the ic3b fragment of the third complement component.	10 41.5 cM	Cell Surface Protein	

AA537404	1.00	-1.18	-0.66	0.85	0.43	1.49	2.74	0.44	2.97	0.34	thymosin beta-10; from rat	AA537404		expressed at relatively high levels in embryonic tissues, and its mRNA is abundant in a variety of tumors and tumor cell lines. a major intracellular g- actin binding protein. (a) plays a significant and possibly obligatory role in cellular processes		Structural Protein	
AA285635	1.00	2.08	-0.32	0.77	3.37	2.34	3.01	1.30	2.95	0.72	ectoplacental cone, invasive trophoblast giant cells, extraembryonic ectoderm and chorion sequence 21; Epc21- pendine	AA285635				EST; Unknown	
Msa.8157.0	1.00	-1.28	-0.93	0.86	0.17	1.94	2.89	0.07	2.95	0.33	cathepsin S; Ctss	AA089333		the cathepsins are mammalian lysosomal cysteine proteinases. they play an important role in protein catabolism within the cell, and may be involved in tumor metastasis	3 42.7 cM	Proteolytic	
D50586	1.00	1.00	0.03	0.57	0.22	1.43	3.12	0.85	2.95	0.33	tissue factor pathway inhibitor 2; Tfp2	D50586			6 1.0 cM		
M74149	1.00	-1.31	-1.11	1.25	0.64	1.77	2.40	0.75	2.94	0.38	creatine kinase, brain; Ckb	M74149	creatine kinase, b chain (ec 2.7.3.2) (b- ck).	reversibly catalyzes the transfer of phosphate between atp and various phosphogens (e.g. creatine phosphate). creatine kinase isoenzymes play a central role in energy transduction in tissues with large, fluctuating energy demands, such as skeletal muscle, heart, brain, and	12 55.0 cM	Metabolic	

Table 1. Summary of protein data bank (PDB) entries

Msa.805.0	1.00	1.60	2.03	1.10	2.06	0.82	1.55	0.25	2.94	1.18	immunoglobulin heavy chain 1 (serum IgG2a),immunoglobulin heavy chain 3 (serum IgG2b),immunoglobulin heavy chain 4 (serum IgG1),immunoglobulin heavy chain 6 (heavy chain of IgM); Igh-1,Igh-3,Igh-4,Igh-5	J00475			12 58.0 cM	Hemostasis	
Msa.7614.0	1.00	-1.36	-0.23	0.68	0.48	1.57	4.41	0.21	2.93	0.49	homolog (84%) of human beta-tubulin	W18778				EST; Unknown	
Msa.3176.0	1.00	1.60	0.10	0.64	1.34	0.17	1.78	0.17	2.91	0.37	cathepsin E; Ctse	X97399	cathepsin e precursor (ec 3.4.23.34).	due to its intracellular location and distribution in lymphoid associated tissue, it may have a role in immune function.	1 69.1 cM	Proteolytic	
X60367-2	1.00	1.25	-0.64	0.89	1.48	0.40	1.75	0.34	2.91	0.22	retinol binding protein 1, cellular; Rbp1	X60367	retinol-binding protein i, cellular (mcrbp).	the rbp1 gene encodes a protein present in a wide variety of adult rat tissues but most abundant in liver and kidney.	9 52.0 cM	Regulatory	
AA542220	1.00	1.33	0.43	1.01	2.01	3.11	3.69	1.55	2.90	0.77	TBX1 protein; TBX1	AA542220	tbx1 protein (t-box protein 1) (testis-specific t-box protein) (fragment).	estrogen treatment resulted in a rapid and transient increase in t-box protein 1 messenger RNA; steady state levels peaked between 2-3 h, returning to basal levels by 6 h. this increase was not abolished by pretreatment with cycloheximide.		Intracellular Protein	
ab000822	1.00	1.09	1.15	0.61	2.65	1.54	3.02	0.68	2.90	0.52	synaptosomal-associated protein, 23kD; Snap23	AB000822			2 61.8 cM		
ab009287	1.00	-1.10	-0.70	0.66	0.26	1.71	2.69	0.03	2.89	0.42	CD68 antigen; Cd68	AB009287	macrosialin precursor (cd68 antigen).	a.k.a macrosialin --the glycoprotein macrosialin is expressed specifically in murine monocytes and macrophages.	11 39.0 cM	Cell Surface Protein	

Table 1. Properties of the proteins

M74227	1.00	-1.62	-1.17	0.88	0.50	1.83	1.58	0.28	2.88	0.15	peptidylprolyl isomerase C; Ppic	M74227	peptidyl-prolyl cis-trans isomerase c (ec 5.2.1.8) (ppiase) (rotamase) (cyclophilin c).	ppases accelerate the folding of proteins.		Intracellular Protein	
Msa.1629.0	1.00	1.00	0.48	1.03	0.32	1.52	2.16	0.22	2.88	0.26	proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional protease 7); Psmb8	U22031	proteasome component c13 precursor (ec 3.4.99.46) (macropain subunit c13) (multicatalytic endopeptidase complex subunit c13).	the proteasome is a multicatalytic proteinase complex which is characterized by its ability to cleave peptides with arg, phe, tyr, leu, and glu adjacent to the leaving group at neutral or slightly basic ph. the proteasome has an atp-dependent proteolytic activity. this subunit may be involved in	17 18.61 cM	Proteolytic	
X04648	1.00	1.05	-0.62	0.83	0.26	2.21	3.17	0.23	2.87	0.37	Fc receptor, IgG, low affinity IIb; Fcgr2b	X04648	low affinity immunoglobulin gamma fc region receptor ii precursor (fc- gamma ii) (fcrit) (igg fc receptor ii beta) (fc gamma receptor iib) (fcgammariib).	a second low affinity receptor for the fc portion of igg. fc\gammarii and fc\gammarii receptors are identical to low affinity receptor for ige on mouse mast cells and macrophages. fc\gammarii is immunologically	1 92.3 cM	Receptor	
M64086	1.00	-1.36	-3.46	4.25	1.63	3.55	4.80	1.51	2.87	0.36	serine protease inhibitor 2-2; Spi2-2	M64086				Proteolytic	
Msa.27449.0	1.00	1.12	-1.53	0.84	0.19	1.58	2.12	0.37	2.87	0.09	secreted phosphoprotein 1; Spp1	AA066782	osteopontin precursor (bone sialoprotein 1) (minopontin) (early t lymphocyte activation 1 protein) (secreted phosphoprotein 1) (spp-1) (2ar) (calcium oxalate crystal growth inhibitor) (osteocalcin)	binds tightly to hydroxyapatite. appears to form an integral part of the mineralized matrix. probably important to cell-matrix interaction.	5 56.0 cM	ECM (Matrix Prot)	
AA140446	1.00	-1.61	-1.09	0.72	0.32	1.85	4.28	2.43	2.84	0.37	DNA segment, Chr 13, Abbott 1 expressed; D13Abbl	AA140446		seven transmembrane domain protein, upregulated during kidney development.	13 6.0 cM	Cell Surface Protein	

AA547057	1.00	1.21	1.69	0.71	1.88	0.13	3.69	0.54	2.83	0.29	ets variant gene 6 (TEL oncogene); ETV6	AA547057	ets-related protein tel (ets translocation variant 6).		6 63.9 cM	Extracellular Protein	
AA259726	1.00	1.02	0.74	0.62	2.33	1.10	3.74	1.63	2.82	0.44	EST; Unknown	AA259726				EST; Unknown	
ET61206	1.00	2.05	1.11	0.76	1.81	0.45	0.70	1.08	2.81	0.31		ET61206				EST; Unknown	
Msa.10497.0	1.00	-4.02	2.16	0.97	0.52	2.77	3.48	2.46	2.79	1.43		W48224					
ET62056	1.00	2.54	-0.61	1.70	1.79	0.33	0.68	1.04	2.78	0.40	immunoglobulin rearranged kappa chain	ET62056				Extracellular Protein	
L06039	1.00	-1.13	0.20	0.74	0.84	2.13	2.78	1.03	2.77	0.13	platelet/endothelial cell adhesion molecule; Pecam	L06039	platelet endothelial cell adhesion molecule precursor (pecam-1) (cd31 antigen).	functions in cell-cell adhesion...expression in lymphocytes transmigration the endothelial cell lining...the function of pecam in the emigration process is not solely to bring leukocytes into contact with the vascular endothelium	6 31.5 cM	Hemostasis	
U90355	1.00	-1.22	-1.48	1.29	0.21	1.62	2.12	0.27	2.77	0.25	fascin homolog 1 (actin bundling protein, Strongylocentrotus purpuratus); Fascin	U90355	fascin.	organizes filamentous actin into bundles with a minimum of 4:1:1 actin/fascin ratio.	5 86.0 cM	Structural Protein	
AA255186	1.00	-1.71	0.71	0.70	0.32	2.47	3.26	0.66	2.76	0.24	cathepsin S; Ctss	AA255186		lysosomal cysteine proteinase	3 42.7 cM	Proteolytic	
AA030649	1.00	-1.29	-0.57	0.54	0.18	2.27	1.99	0.28	2.76	0.51	procollagen, type V, alpha 1; Col5a1	AA030649		type v collagen is a member of group i collagen (fibrillar forming collagen). collagen v is expressed in connective tissue in close contact with the vascular basement membrane in bone, skin, cartilage, tendon, connective tissue	2 18.0 cM	ECM (Matrix Prot)	
Msa.544.0	1.00	-2.55	-3.78	2.77	-0.05	1.74	1.98	0.15	2.75	0.27	procollagen, type V, alpha 2; Col5a2	L02918				ECM (Matrix Prot)	
AA690738	1.00	-1.06	0.68	0.56	1.54	0.10	2.40	0.32	2.74	0.47	EST; Unknown	AA690738				EST; Unknown	
AA711271	1.00	-1.70	-0.60	0.75	0.81	2.07	3.05	1.23	2.73	0.39	EST; Unknown	AA711271				EST; Unknown	

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Table 1. Summary of the data for the 10 proteins.

Accession	Gene	Protein	Length (aa)	pI	pI ₂	pI ₃	pI ₄	pI ₅	pI ₆	pI ₇	pI ₈	pI ₉	pI ₁₀	pI ₁₁	pI ₁₂	pI ₁₃	pI ₁₄	pI ₁₅	pI ₁₆	pI ₁₇	pI ₁₈	pI ₁₉	pI ₂₀	pI ₂₁	pI ₂₂	pI ₂₃	pI ₂₄	pI ₂₅	pI ₂₆	pI ₂₇	pI ₂₈	pI ₂₉	pI ₃₀	pI ₃₁	pI ₃₂	pI ₃₃	pI ₃₄	pI ₃₅	pI ₃₆	pI ₃₇	pI ₃₈	pI ₃₉	pI ₄₀	pI ₄₁	pI ₄₂	pI ₄₃	pI ₄₄	pI ₄₅	pI ₄₆	pI ₄₇	pI ₄₈	pI ₄₉	pI ₅₀	pI ₅₁	pI ₅₂	pI ₅₃	pI ₅₄	pI ₅₅	pI ₅₆	pI ₅₇	pI ₅₈	pI ₅₉	pI ₆₀	pI ₆₁	pI ₆₂	pI ₆₃	pI ₆₄	pI ₆₅	pI ₆₆	pI ₆₇	pI ₆₈	pI ₆₉	pI ₇₀	pI ₇₁	pI ₇₂	pI ₇₃	pI ₇₄	pI ₇₅	pI ₇₆	pI ₇₇	pI ₇₈	pI ₇₉	pI ₈₀	pI ₈₁	pI ₈₂	pI ₈₃	pI ₈₄	pI ₈₅	pI ₈₆	pI ₈₇	pI ₈₈	pI ₈₉	pI ₉₀	pI ₉₁	pI ₉₂	pI ₉₃	pI ₉₄	pI ₉₅	pI ₉₆	pI ₉₇	pI ₉₈	pI ₉₉	pI ₁₀₀	pI ₁₀₁	pI ₁₀₂	pI ₁₀₃	pI ₁₀₄	pI ₁₀₅	pI ₁₀₆	pI ₁₀₇	pI ₁₀₈	pI ₁₀₉	pI ₁₁₀	pI ₁₁₁	pI ₁₁₂	pI ₁₁₃	pI ₁₁₄	pI ₁₁₅	pI ₁₁₆	pI ₁₁₇	pI ₁₁₈	pI ₁₁₉	pI ₁₂₀	pI ₁₂₁	pI ₁₂₂	pI ₁₂₃	pI ₁₂₄	pI ₁₂₅	pI ₁₂₆	pI ₁₂₇	pI ₁₂₈	pI ₁₂₉	pI ₁₃₀	pI ₁₃₁	pI ₁₃₂	pI ₁₃₃	pI ₁₃₄	pI ₁₃₅	pI ₁₃₆	pI ₁₃₇	pI ₁₃₈	pI ₁₃₉	pI ₁₄₀	pI ₁₄₁	pI ₁₄₂	pI ₁₄₃	pI ₁₄₄	pI ₁₄₅	pI ₁₄₆	pI ₁₄₇	pI ₁₄₈	pI ₁₄₉	pI ₁₅₀	pI ₁₅₁	pI ₁₅₂	pI ₁₅₃	pI ₁₅₄	pI ₁₅₅	pI ₁₅₆	pI ₁₅₇	pI ₁₅₈	pI ₁₅₉	pI ₁₆₀	pI ₁₆₁	pI ₁₆₂	pI ₁₆₃	pI ₁₆₄	pI ₁₆₅	pI ₁₆₆	pI ₁₆₇	pI ₁₆₈	pI ₁₆₉	pI ₁₇₀	pI ₁₇₁	pI ₁₇₂	pI ₁₇₃	pI ₁₇₄	pI ₁₇₅	pI ₁₇₆	pI ₁₇₇	pI ₁₇₈	pI ₁₇₉	pI ₁₈₀	pI ₁₈₁	pI ₁₈₂	pI ₁₈₃	pI ₁₈₄	pI ₁₈₅	pI ₁₈₆	pI ₁₈₇	pI ₁₈₈	pI ₁₈₉	pI ₁₉₀	pI ₁₉₁	pI ₁₉₂	pI ₁₉₃	pI ₁₉₄	pI ₁₉₅	pI ₁₉₆	pI ₁₉₇	pI ₁₉₈	pI ₁₉₉	pI ₂₀₀	pI ₂₀₁	pI ₂₀₂	pI ₂₀₃	pI ₂₀₄	pI ₂₀₅	pI ₂₀₆	pI ₂₀₇	pI ₂₀₈	pI ₂₀₉	pI ₂₁₀	pI ₂₁₁	pI ₂₁₂	pI ₂₁₃	pI ₂₁₄	pI ₂₁₅	pI ₂₁₆	pI ₂₁₇	pI ₂₁₈	pI ₂₁₉	pI ₂₂₀	pI ₂₂₁	pI ₂₂₂	pI ₂₂₃	pI ₂₂₄	pI ₂₂₅	pI ₂₂₆	pI ₂₂₇	pI ₂₂₈	pI ₂₂₉	pI ₂₃₀	pI ₂₃₁	pI ₂₃₂	pI ₂₃₃	pI ₂₃₄	pI ₂₃₅	pI ₂₃₆	pI ₂₃₇	pI ₂₃₈	pI ₂₃₉	pI ₂₄₀	pI ₂₄₁	pI ₂₄₂	pI ₂₄₃	pI ₂₄₄	pI ₂₄₅	pI ₂₄₆	pI ₂₄₇	pI ₂₄₈	pI ₂₄₉	pI ₂₅₀	pI ₂₅₁	pI ₂₅₂	pI ₂₅₃	pI ₂₅₄	pI ₂₅₅	pI ₂₅₆	pI ₂₅₇	pI ₂₅₈	pI ₂₅₉	pI ₂₆₀	pI ₂₆₁	pI ₂₆₂	pI ₂₆₃	pI ₂₆₄	pI ₂₆₅	pI ₂₆₆	pI ₂₆₇	pI ₂₆₈	pI ₂₆₉	pI ₂₇₀	pI ₂₇₁	pI ₂₇₂	pI ₂₇₃	pI ₂₇₄	pI ₂₇₅	pI ₂₇₆	pI ₂₇₇	pI ₂₇₈	pI ₂₇₉	pI ₂₈₀	pI ₂₈₁	pI ₂₈₂	pI ₂₈₃	pI ₂₈₄	pI ₂₈₅	pI ₂₈₆	pI ₂₈₇	pI ₂₈₈	pI ₂₈₉	pI ₂₉₀	pI ₂₉₁	pI ₂₉₂	pI ₂₉₃	pI ₂₉₄	pI ₂₉₅	pI ₂₉₆	pI ₂₉₇	pI ₂₉₈	pI ₂₉₉	pI ₃₀₀	pI ₃₀₁	pI ₃₀₂	pI ₃₀₃	pI ₃₀₄	pI ₃₀₅	pI ₃₀₆	pI ₃₀₇	pI ₃₀₈	pI ₃₀₉	pI ₃₁₀	pI ₃₁₁	pI ₃₁₂	pI ₃₁₃	pI ₃₁₄	pI ₃₁₅	pI ₃₁₆	pI ₃₁₇	pI ₃₁₈	pI ₃₁₉	pI ₃₂₀	pI ₃₂₁	pI ₃₂₂	pI ₃₂₃	pI ₃₂₄	pI ₃₂₅	pI ₃₂₆	pI ₃₂₇	pI ₃₂₈	pI ₃₂₉	pI ₃₃₀	pI ₃₃₁	pI ₃₃₂	pI ₃₃₃	pI ₃₃₄	pI ₃₃₅	pI ₃₃₆	pI ₃₃₇	pI ₃₃₈	pI ₃₃₉	pI ₃₄₀	pI ₃₄₁	pI ₃₄₂	pI ₃₄₃	pI ₃₄₄	pI ₃₄₅	pI ₃₄₆	pI ₃₄₇	pI ₃₄₈	pI ₃₄₉	pI ₃₅₀	pI ₃₅₁	pI ₃₅₂	pI ₃₅₃	pI ₃₅₄	pI ₃₅₅	pI ₃₅₆	pI ₃₅₇	pI ₃₅₈	pI ₃₅₉	pI ₃₆₀	pI ₃₆₁	pI ₃₆₂	pI ₃₆₃	pI ₃₆₄	pI ₃₆₅	pI ₃₆₆	pI ₃₆₇	pI ₃₆₈	pI ₃₆₉	pI ₃₇₀	pI ₃₇₁	pI ₃₇₂	pI ₃₇₃	pI ₃₇₄	pI ₃₇₅	pI ₃₇₆	pI ₃₇₇	pI ₃₇₈	pI ₃₇₉	pI ₃₈₀	pI ₃₈₁	pI ₃₈₂	pI ₃₈₃	pI ₃₈₄	pI ₃₈₅	pI ₃₈₆	pI ₃₈₇	pI ₃₈₈	pI ₃₈₉	pI ₃₉₀	pI ₃₉₁	pI ₃₉₂	pI ₃₉₃	pI ₃₉₄	pI ₃₉₅	pI ₃₉₆	pI ₃₉₇	pI ₃₉₈	pI ₃₉₉	pI ₄₀₀	pI ₄₀₁	pI ₄₀₂	pI ₄₀₃	pI ₄₀₄	pI ₄₀₅	pI ₄₀₆	pI ₄₀₇	pI ₄₀₈	pI ₄₀₉	pI ₄₁₀	pI ₄₁₁	pI ₄₁₂	pI ₄₁₃	pI ₄₁₄	pI ₄₁₅	pI ₄₁₆	pI ₄₁₇	pI ₄₁₈	pI ₄₁₉	pI ₄₂₀	pI ₄₂₁	pI ₄₂₂	pI ₄₂₃	pI ₄₂₄	pI ₄₂₅	pI ₄₂₆	pI ₄₂₇	pI ₄₂₈	pI ₄₂₉	pI ₄₃₀	pI ₄₃₁	pI ₄₃₂	pI ₄₃₃	pI ₄₃₄	pI ₄₃₅	pI ₄₃₆	pI ₄₃₇	pI ₄₃₈	pI ₄₃₉	pI ₄₄₀	pI ₄₄₁	pI ₄₄₂	pI ₄₄₃	pI ₄₄₄	pI ₄₄₅	pI ₄₄₆	pI ₄₄₇	pI ₄₄₈	pI ₄₄₉	pI ₄₅₀	pI ₄₅₁	pI ₄₅₂	pI ₄₅₃	pI ₄₅₄	pI ₄₅₅	pI ₄₅₆	pI ₄₅₇	pI ₄₅₈	pI ₄₅₉	pI ₄₆₀	pI ₄₆₁	pI ₄₆₂	pI ₄₆₃	pI ₄₆₄	pI ₄₆₅	pI ₄₆₆	pI ₄₆₇	pI ₄₆₈	pI ₄₆₉	pI ₄₇₀	pI ₄₇₁	pI ₄₇₂	pI ₄₇₃	pI ₄₇₄	pI ₄₇₅	pI ₄₇₆	pI ₄₇₇	pI ₄₇₈	pI ₄₇₉	pI ₄₈₀	pI ₄₈₁	pI ₄₈₂	pI ₄₈₃	pI ₄₈₄	pI ₄₈₅	pI ₄₈₆	pI ₄₈₇	pI ₄₈₈	pI ₄₈₉	pI ₄₉₀	pI ₄₉₁	pI ₄₉₂	pI ₄₉₃	pI ₄₉₄	pI ₄₉₅	pI ₄₉₆	pI ₄₉₇	pI ₄₉₈	pI ₄₉₉	pI ₅₀₀	pI ₅₀₁	pI ₅₀₂	pI ₅₀₃	pI ₅₀₄	pI ₅₀₅	pI ₅₀₆	pI ₅₀₇	pI ₅₀₈	pI ₅₀₉	pI ₅₁₀	pI ₅₁₁	pI ₅₁₂	pI ₅₁₃	pI ₅₁₄	pI ₅₁₅	pI ₅₁₆	pI ₅₁₇	pI ₅₁₈	pI ₅₁₉	pI ₅₂₀	pI ₅₂₁	pI ₅₂₂	pI ₅₂₃	pI ₅₂₄	pI ₅₂₅	pI ₅₂₆	pI ₅₂₇	pI ₅₂₈	pI ₅₂₉	pI ₅₃₀	pI ₅₃₁	pI ₅₃₂	pI ₅₃₃	pI ₅₃₄	pI ₅₃₅	pI ₅₃₆	pI ₅₃₇	pI ₅₃₈	pI ₅₃₉	pI ₅₄₀	pI ₅₄₁	pI ₅₄₂	pI ₅₄₃	pI ₅₄₄	pI ₅₄₅	pI ₅₄₆	pI ₅₄₇	pI ₅₄₈	pI ₅₄₉	pI ₅₅₀	pI ₅₅₁	pI ₅₅₂	pI ₅₅₃	pI ₅₅₄	pI ₅₅₅	pI ₅₅₆	pI ₅₅₇	pI ₅₅₈	pI ₅₅₉	pI ₅₆₀	pI ₅₆₁	pI ₅₆₂	pI ₅₆₃	pI ₅₆₄	pI ₅₆₅	pI ₅₆₆	pI ₅₆₇	pI ₅₆₈	pI ₅₆₉	pI ₅₇₀	pI ₅₇₁	pI ₅₇₂	pI ₅₇₃	pI ₅₇₄	pI ₅₇₅	pI ₅₇₆	pI ₅₇₇	pI ₅₇₈	pI ₅₇₉	pI ₅₈₀	pI ₅₈₁	pI ₅₈₂	pI ₅₈₃	pI ₅₈₄	pI ₅₈₅	pI ₅₈₆	pI ₅₈₇	pI ₅₈₈	pI ₅₈₉	pI ₅₉₀	pI ₅₉₁	pI ₅₉₂	pI ₅₉₃	pI ₅₉₄	pI ₅₉₅	pI ₅₉₆	pI ₅₉₇	pI ₅₉₈	pI ₅₉₉	pI ₆₀₀	pI ₆₀₁	pI ₆₀₂	pI ₆₀₃	pI ₆₀₄	pI ₆₀₅	pI ₆₀₆	pI ₆₀₇	pI ₆₀₈	pI ₆₀₉	pI ₆₁₀	pI ₆₁₁	pI ₆₁₂	pI ₆₁₃	pI ₆₁₄	pI ₆₁₅	pI ₆₁₆	pI ₆₁₇	pI ₆₁₈	pI ₆₁₉	pI ₆₂₀	pI ₆₂₁	pI ₆₂₂	pI ₆₂₃	pI ₆₂₄	pI ₆₂₅	pI ₆₂₆	pI ₆₂₇	pI ₆₂₈	pI ₆₂₉	pI ₆₃₀	pI ₆₃₁	pI ₆₃₂	pI ₆₃₃	pI ₆₃₄	pI ₆₃₅	pI ₆₃₆	pI ₆₃₇	pI ₆₃₈	pI ₆₃₉	pI ₆₄₀	pI ₆₄₁	pI ₆₄₂	pI ₆₄₃	pI ₆₄₄	pI ₆₄₅	pI ₆₄₆	pI ₆₄₇	pI ₆₄₈	pI ₆₄₉	pI ₆₅₀	pI ₆₅₁	pI ₆₅₂	pI ₆₅₃	pI ₆₅₄	pI ₆₅₅	pI ₆₅₆	pI ₆₅₇	pI ₆₅₈	pI ₆₅₉	pI ₆₆₀	pI ₆₆₁	pI ₆₆₂	pI ₆₆₃	pI ₆₆₄	pI ₆₆₅	pI ₆₆₆	pI ₆₆₇	pI ₆₆₈	pI ₆₆₉	pI ₆₇₀	pI ₆₇₁	pI ₆₇₂	pI ₆₇₃	pI ₆₇₄	pI ₆₇₅	pI ₆₇₆	pI ₆₇₇	pI ₆₇₈	pI ₆₇₉	pI ₆₈₀	pI ₆₈₁	pI ₆₈₂	pI ₆₈₃	pI ₆₈₄	pI ₆₈₅	pI ₆₈₆	pI ₆₈₇	pI ₆₈₈	pI ₆₈₉	pI ₆₉₀	pI ₆₉₁	pI ₆₉₂	pI ₆₉₃	pI ₆₉₄	pI ₆₉₅	pI ₆₉₆	pI ₆₉₇	pI ₆₉₈	pI ₆₉₉	pI ₇₀₀	pI ₇₀₁	pI ₇₀₂	pI ₇₀₃	pI ₇₀₄	pI ₇₀₅	pI ₇₀₆	pI ₇₀₇	pI ₇₀₈	pI ₇₀₉	pI ₇₁₀	pI ₇₁₁	pI ₇₁₂	pI ₇₁₃	pI ₇₁₄	pI ₇₁₅	pI ₇₁₆	pI ₇₁₇	pI ₇₁₈	pI ₇₁₉	pI ₇₂₀	pI ₇₂₁	pI ₇₂₂	pI ₇₂₃	pI ₇₂₄	pI ₇₂₅	pI 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Table 1. Summary of the data obtained from the microarray analysis of the gene expression profile of the cells treated with the anti-CD44 antibody.

Gene	1.00	-1.00	0.51	0.62	1.60	0.49	2.18	0.08	2.56	0.29	cathepsin H; Ctsh	U06119	cathepsin h precursor (cc 3.4.22.16) (cathepsin b3) (cathepsin ba).	activation of macrophages by gamma-interferon induces expression of major histocompatibility complex (mhc) class ii genes. an increase in cathepsin h, encoded in the mouse by ctsh, is also induced by gamma-interferon and is associated with a role in fibrillogenesis by controlling lateral growth of collagen ii fibrils.	9 50.0 cM	Proteolytic	
D38162	1.00	-2.75	-1.55	0.62	-0.14	1.74	0.58	1.10	2.54	0.31	procollagen, type XI, alpha 1; Col11a1	D38162	collagen alpha 1(x1) chain precursor.	may play an important role in fibrillogenesis by controlling lateral growth of collagen ii fibrils.	3 53.1 cM	ECM (Matrix Prot)	
AA108054	1.00	-1.40	-0.41	0.50	1.29	0.21	1.78	0.28	2.53	0.24	serine protease inhibitor 6; Spi6	AA108054			13 16.0 cM		
U56819	1.00	-1.28	0.64	0.60	0.83	1.98	4.27	0.29	2.53	0.17	chemokine (C-C) receptor 2; Cmrbr2	U56819	c-c chemokine receptor type 2 (c-c ckr-2) (cc-ckr-2) (ccr-2) (ccr2) (je/fic receptor) (mcp-1 receptor).	receptor for the mcp-1 (je), mcp-3 (fic) and mcp-5 chemokines. transduces a signal by increasing the intracellular calcium ions level	9 72.0 cM		
Msa.16995.0	1.00	-1.11	-2.58	2.64	-0.12	1.95	3.20	0.17	2.52	0.46	arachidonate 5-lipoxygenase activating protein	W83564		seems to be required for the activation of 5-lipoxygenase. flap could play an essential role in the transfer of arachidonic acid to 5-lipo. flap binds to mk-886, a compound that blocks the biosynthesis of leukotrienes		Intracellular Protein	
Msa.88.0	1.00	-2.30	-4.15	2.92	0.09	2.23	1.91	0.28	2.52	0.21	osteoblast specific factor 2; OSF-2	D13664		preferentially expressed in periosteum and periodontal ligament. involved in cell adhesion, highly homologous to beta-actin, a molecule induced by transforming growth factor beta (tgf-beta) that promotes the differentiation of osteoblasts		Extracellular Protein	

U92437	1.00	-1.85	1.71	0.67	2.06	0.03	2.72	0.35	2.48	0.28	phosphatase and tensin homolog; Pten	U92437	protein-tyrosine phosphatase pten (ec 3.1.3.48) (mutated in multiple advanced cancers)	potential tumor suppressor. active as a phosphatase on tyrosine, serine and threonine residues. no match on blast search 1/99.	19 24.5 cM		
AA667371	1.00	-2.99	-1.56	0.83	-0.40	2.70	0.68	0.93	2.42	0.25	Unknown	AA667371	growth arrest and dna-damage-inducible protein gadd45 gamma (cytokine responsive protein cr6).	plays an important role in negative growth control, including both growth suppression and apoptosis.		EST; Unknown	
Msa.7498.0	1.00	1.38	-0.01	1.13	0.49	1.77	2.90	0.20	2.41	0.37	growth arrest and DNA-damage-inducible, gamma; Gadd45g	AA138777	transcription factor maf2 (proto-oncogene c-maf).			Regulatory	
S74567	1.00	-1.41	3.30	0.41	2.84	1.39	2.88	0.80	2.39	1.21	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog; Maf	S74567	growth arrest and dna-damage-inducible protein gadd45.	the c-maf interaction site was mapped to the sequence 5'-[gt]g[gc]n[gt]nctcagnn-3' in the 17 promoter. it may interact with additional basic-zipper proteins that determine a subtype of maf-responsive element binding.	8 61.0 cM		
AA238081	1.00	-1.19	-1.01	1.19	0.78	2.13	2.04	0.37	2.39	0.24	complement component 1, r subcomponent; C1r	AA238081	myristoylated alanine rich protein kinase C substrate; Macs		6		
W53443	1.00	1.39	-1.66	1.86	0.32	1.35	1.74	0.34	2.38	0.13	GENESEQ:V34267 Human secreted protein gene 58 clone HSSEP68.	W53443	myristoylated alanine rich protein kinase C substrate; Macs	also a good match to human clone 2491 (af131781) (both are 89%)		EST; Unknown	
L28177	1.00	1.22	-0.67	1.07	0.03	1.44	5.51	0.19	2.36	0.44	DNA-damage inducible transcript 1; Ddit1	L28177	growth arrest and dna-damage-inducible protein gadd45.	binds to proliferating cell nuclear antigen. might affect p53 interaction with some cdk (cell division protein kinase) complexes; stimulates dna excision repair in vitro and inhibits entry of cells into S phase.	3 70.5 cM	Intracellular Protein	
Msa.928.0	1.00	-1.07	-1.99	1.35	0.25	1.47	1.88	0.09	2.35	0.18	myristoylated alanine rich protein kinase C substrate; Macs	M60474	myristoylated alanine-rich c-kinase substrate (marcks).	marcks is the most prominent cellular substrate for protein kinase c. this protein binds calmodulin, actin, and synapsin. marcks is a filamentous (f) actin cross-linking protein.	10 22.0 cM	Structural Protein	

Table 1. Properties of the proteins

AA475111	1.00	-1.27	1.20	0.45	1.54	0.12	2.49	0.30	2.31	0.19	heterogeneous nuclear ribonucleoprotein D-EST; Unknown	AA475111					
AA536849	1.00	-1.97	0.31	0.73	3.28	1.85	2.32	0.71	2.31	0.51	EST; Unknown	AA536849					EST; Unknown
C81524	1.00	-1.20	2.02	0.85	1.09	2.55	1.96	1.84	2.31	1.29		C81524					
AA170245	1.00	1.08	0.79	0.45	0.60	1.69	2.32	0.10	2.30	0.18		AA170245					
AF013262	1.00	-2.69	-0.93	0.72	1.19	2.74	2.01	0.60	2.30	0.72	lumican; Lum	AF013262	lumican precursor (lum) (keratan sulfate proteoglycan).	leucine-rich proteoglycan with keratan sulfate side chains, a major component of cornea, dermal, and muscle connective tissues. regulation of collagen assembly into fibrils in various connective tissues. lumican is necessary in the development of the cornea.	10 61.0 cM	ECM (Matrix Prot)	
AF020313	1.00	-1.73	0.47	0.68	1.07	2.46	3.40	1.07	2.30	0.16	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein; Apbb1ip-binding	AF020313				Extracellular Protein	
Msa.22488.0	1.00	1.08	-1.88	1.54	0.27	2.19	2.75	0.57	2.30	0.22	cathepsin S; Ctss	AA146437		the cathepsins are mammalian lysosomal cysteine proteinases. they play an important role in protein catabolism within the cell, and may be involved in tumor metastasis.	3 42.7 cM	Proteolytic	
AF004666	1.00	1.09	0.15	0.48	0.11	1.17	2.68	0.32	2.27	0.40	solute carrier family 8 (sodium/calcium exchanger), member 1; Slc8a1	AF004666	sodium/calcium exchanger 1 precursor (na+/ca2+-exchange protein 1).	rapidly transports ca2+ during excitation-contraction coupling. ca(2+) is extruded from the cell during relaxation so as to prevent overloading of intracellular stores	17 48.0 cM		
Msa.1171.0	1.00	0.63	-0.50	0.61	0.72	2.71	-0.69	1.03	2.27	2.79	keratin-associated protein 5-4; Krtap5-4	M37760					

Table 1. Properties of the lectins

Msa.	683.0	1.00	-1.85	-0.89	1.02	0.31	1.63	2.14	0.05	2.25	0.17	lectin, galactose binding, soluble 1; Lgals1	W13002	galactin-1 (beta-galactoside-binding lectin 1-14-i) (lactose-binding lectin 1) (s-lac lectin 1) (galaptin) (14 kda lectin).	postimplantation, Lgals1 is expressed in somite myotomes, suggesting a role in muscle development. this protein binds beta-galactoside. its physiological function is not yet known. it may act as an autocrine negative growth factor that causes endopeptidase.	15 44.9 cM	Other	
Msa.	5619.0	1.00	-1.16	-3.48	2.53	-0.07	2.03	2.48	0.33	2.22	0.22	protease, cysteine, 1; Prsc1	AA000961		a cysteine endopeptidase. legumain was found in all mouse tissues examined, but was particularly abundant in kidney and placenta. the distribution in subcellular fractions of mouse and rat kidney showed a		Proteolytic	
AA119603		1.00	1.13	1.06	0.58	1.58	0.16	2.17	0.13	2.22	0.30	L1 repeat, Tf	AA119603					
D84391		1.00	-1.58	1.92	0.91	2.05	0.87	1.83	1.73	2.21	1.32	subfamily, member 14, L1 repeat, Tf subfamily, member 29; LIMd-Tf14.1LMd-Tf29	D84391				EST; Unknown	
X16874		1.00	-1.38	-1.89	2.31	0.25	1.88	2.10	0.00	2.17	0.18	complement component 1, q subcomponent, beta polypeptide; C1qb	X16874	complement c1q subcomponent, b chain precursor.	the primary humoral mediator of antigen-antibody reactions is the complement (c) system.	4 66.1 cM	Hemostasis	
AF022992		1.00	4.47	1.39	0.28	0.21	1.33	1.55	1.17	2.16	0.30	period homolog (Drosophila); Per	AF022992	per-hexamer repeat protein 5, period circadian protein 1 (circadian pacemaker protein ritm1) (mmer) (m-	circadian regulator that may act as a transcription factor. behaves as a negative element in circadian transcriptional loop.	11 B	Other	

Table 1. Properties of uncoupling protein 2 (ucp2) and its isoforms.

Accession	1.00	1.15	-7.17	7.77	1.42	0.28	2.76	0.71	2.16	0.11	uncoupling protein 2, mitochondrial; Ucp2	U69135	mitochondrial uncoupling protein 2 (ucp 2) (ucph)	ucp are mitochondrial transporter proteins that create proton leaks across the inner mitochondrial membrane, thus uncoupling oxidative phosphorylation from atp synthesis. as a result, energy is dissipated in the form of heat	750.0 cM	Intracellular Protein	
Msa.4530.0	1.00	1.34	0.13	0.56	1.33	0.21	2.22	0.10	2.16	0.41	EST; region of homology to GENESEQN:Z77537 Human ovarian tumor cDNA library derived EST fragment 88	AA106931				EST; Unknown	
Msa.34975.0	1.00	3.11	1.82	0.58	1.92	0.83	2.57	0.42	2.14	0.22	eukaryotic translation initiation factor 2, structural gene Y-linked; Eif2s3y	AA118716	eukaryotic translation initiation factor 2 gamma subunit y-linked (eif2-gamma y).	eif-2 functions in the early steps of protein synthesis by forming a ternary complex with gtp and initiator tma. this complex binds to a 4s ribosomal subunit, followed by mrna binding to form a 43s preinitiation complex. junction of the 6s ribosomal subunit to form the 8s initiation complex is preceded by hydrolysis of the gtp bound to eif-2 and release of an eif-2-gdp binary complex. in order for eif-2 to recycle and catalyze another round of initiation, the gdp bound to eif-2 must exchange with gtp by way of a reaction catalyzed by eif-2b (by	Y	Regulatory	
AA616077	1.00	-1.88	-0.15	0.53	1.56	0.52	2.53	0.27	2.13	0.17		AA616077				EST; Unknown	
AA607513	1.00	-3.27	-3.57	2.01	-0.15	2.43	0.84	0.96	2.13	0.33	Unknown	AA607513				EST; Unknown	
ET62894	1.00	-3.02	0.12	0.95	0.03	1.39	1.03	1.20	2.09	0.16		ET62894				EST; Unknown	

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U31993	1.00	1.00	-0.75	0.59	0.42	1.89	2.35	0.25	2.08	0.24	interleukin 17 receptor; IL17r	U31993				6 55.2 cM	Receptor	
Msa.9251.0	1.00	-1.29	-1.33	0.91	0.29	1.90	2.56	0.10	2.05	0.37	neutrophil cytosolic factor 2; Ncf2	AA050149				1 76.1 cM	Intracellular Protein	
Msa.978.0	1.00	-1.00	-1.30	1.35	0.07	1.36	2.07	0.05	2.04	0.24	moesin; Msn	M86390	moesin (membrane-organizing extension spike protein).	thought to work as cross-linkers between plasma membranes and actin-based cytoskeletons. these molecules are involved not only in cytoskeletal organization but also in signal transduction.	X	Cell Surface Protein		
AA474881	1.00	-1.06	1.37	0.61	1.85	0.05	2.66	0.28	2.01	0.20	DNA segment, Chr 1, Wayne State University 40, expressed.	AA474881			1 17.0 cM			
AA204590	1.00	-1.39	0.50	0.54	0.11	1.23	3.51	0.74	2.01	0.31	EST; Unknown	AA204590					EST; Unknown	
AA691533	1.00	-7.45	-1.37	0.88	0.56	2.15	0.50	0.96	2.00	0.50		AA691533					EST; Unknown	
Msa.17862.0	1.00	-6.92	-1.98	0.96	-0.02	1.49	1.85	0.27	1.99	0.12	lysyl oxidase-like; Loxl	W98413				9 33.0 cM		
Msa.29217.0	1.00	-3.11	-1.61	3.81	1.65	0.59	2.80	0.79	1.96	0.30	actin, beta, cytoplasmic	AA079937					Structural Protein	
Msa.24381.0	1.00	-2.44	0.70	0.66	0.52	1.55	2.40	0.55	1.92	0.35	damage specific DNA binding protein 1 (127 kDa); Ddb1	W42399		a dna binding protein that binds specifically to damaged dna. a defect in binding activity is associated with xeroderma pigmentosum e (xpe) in humans	19 5.0 cM	Other		
X57337	1.00	-2.45	-1.87	0.89	-0.11	1.76	1.39	0.13	1.91	0.19	procollagen C-proteinase enhancer protein; Pcolce	X57337	procollagen c-proteinase enhancer protein precursor (pcpe) (type i procollagen coo-terminal proteinase enhancer) (type 1 procollagen c-proteinase enhancer protein) (h14)	a glycoprotein that potentiates enzymatic cleavage of the type i procollagen c-propeptide by bone morphogenetic protein-1 (bmp-1)	5 78.0 cM	Extracellular Protein		
Msa.2924.0	1.00	-1.06	-0.71	0.56	0.35	1.36	2.66	0.30	1.91	0.27	superoxide dismutase 3, extracellular; Sod3	X84940	extracellular superoxide dismutase [cu-zn] precursor (ec 1.15.1.1) (ec-sod).	destroys radicals which are normally produced within the cells and are toxic to biological systems.	5 31.0 cM			
AA608277	1.00	1.72	0.73	0.50	1.21	0.03	2.36	0.18	1.91	0.42		AA608277						

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Table 1. Summary of protein properties and functions.

U75530	1.00	-1.41	3.24	1.00	0.89	2.65	1.99	3.07	1.90	1.73	eukaryotic translation initiation factor 4E binding protein 2; Eif4ebp2	U75530			10 32.0 cM		
M91380	1.00	-2.56	-2.42	1.30	-0.27	1.66	1.64	0.21	1.89	0.10	follistatin-like; Fstl1	M91380	follistatin-related protein precursor (tgf-beta-inducible protein tsc-36).	tgfb responsive gene cloned from an osteoblastic cell line. encodes a protein of 35 kda. the amino acid sequence of tsc-36 protein was found to be similar to follistatin, an activin-binding protein, also similar to the secreted	16 27.3 cM	Extracellular Protein	
Msa.21961.0	1.00	-2.48	-0.32	0.79	-0.12	1.13	1.58	0.25	1.89	0.26	EST; Unknown	AA030421		est		EST; Unknown	
Z31334	1.00	-2.57	-3.02	1.52	-0.47	1.96	0.49	0.81	1.84	0.12	procollagen, type I, alpha 2, Cola2	Z31334	collagen alpha 2(i) chain precursor.	type i collagen, the commonest form, is a fibrillar collagen, along with types ii, iii, v. and xi	6 0.68 cM	ECM (Matrix Prot)	
AA176016	1.00	-2.13	0.89	0.73	1.69	0.05	2.43	0.32	1.82	0.19		AA176016					
AA510381	1.00	1.29	1.66	0.99	0.08	1.75	1.14	1.51	1.82	1.19		AA510381					
AA146539	1.00	-1.05	1.80	0.52	1.91	0.05	2.13	0.31	1.78	0.07	EGF-like repeats and discordin I-like domains 3; Edil3	AA146539					
Msa.2536.0	1.00	2.69	-0.19	0.81	1.43	0.08	1.88	0.57	1.74	0.20	extracellular proteinase inhibitor; Expi	X93037	wdnm1 protein precursor.	could have proteinase inhibiting capacity.			
D78188	1.00	-2.03	0.04	0.66	0.34	2.02	1.82	0.41	1.74	0.26	granule cell differentiation protein; Gcdp	D78188	myotrophin (v-l protein) (granule cell differentiation protein).	potential role in cerebellar morphogenesis. may function in differentiation of cerebellar neurons, particularly of granule cells			
X93037	1.00	3.54	-0.36	0.70	1.60	0.26	1.81	0.49	1.73	0.20	extracellular proteinase inhibitor; Expi	X93037	wdnm1 protein precursor.	could have proteinase inhibiting capacity.			

D50460	1.00	-3.16	-1.78	0.97	0.21	1.47	0.41	0.87	1.67	0.15	stromal cell derived factor 3; Sdf3	D50460	pigment epithelium-derived factor (pedf) (stromal cell-derived factor 3) (sdf-3).	a.k.a pigment epithelium-derived factor -- a member of the serine protease inhibitor (serpin) superfamily, promotes survival and/or differentiation of rat cerebellar granule neurons and human retinoblastoma cells in vitro. no inhibitory effect.		Cytokine	
C76162	1.00	-2.16	0.93	0.55	1.90	0.72	1.59	0.29	1.66	0.22		C76162					
Msa.27482.0	1.00	-2.98	-0.34	0.93	-0.02	1.68	0.79	0.95	1.63	0.09	DNA segment, Chr 10, Johns Hopkins University 81 expressed; D10Jhu81e	AA139094			10 41.7 cM		
X65582	1.00	-2.34	-2.58	0.91	-0.22	1.62	0.31	0.86	1.63	0.20	procollagen, type VI, alpha 2; Col6a2	X65582	collagen alpha 2(vi) chain precursor.	collagen vi acts as a cell-binding protein.	10 41.1 cM	ECM (Matrix Prot)	
X58251	1.00	-2.11	-0.18	0.74	0.01	1.14	0.61	0.89	1.62	0.20	procollagen, type I, alpha 2; Cola2	X58251	collagen alpha 2(i) chain precursor.	forms the fibrils of tendon, ligaments and bones. in bones the fibrils are mineralized with calcium hydroxyapatite.	6 0.68 cM	ECM (Matrix Prot)	
Msa.22727.0	1.00	-2.67	-0.62	2.27	0.42	1.67	1.45	1.31	1.61	0.93	melanoma X-actin; Actx	AA038134				Structural Protein	
X66405	1.00	-2.18	-3.12	1.32	-0.39	1.72	-0.54	0.85	1.53	0.22	procollagen, type VI, alpha 1; Col6a1	X66405	collagen alpha 1(vi) chain precursor.	collagen vi acts as a cell-binding protein.	10 41.1 cM	ECM (Matrix Prot)	
AF022256	1.00	-3.92	-1.46	0.47	-0.36	1.65	-1.65	1.42	1.49	0.18	keratocan; Kera	AF022256		keratan sulfate proteoglycans (kspgs) play a pivotal role in the development and maintenance of corneal transparency. keratocan, lumican, and mimecan (osteoglycin) are the major keratins in	10 61.0 cM	ECM (Matrix Prot)	
Msa.22485.0	1.00	-2.42	-0.72	0.53	1.18	0.18	1.79	0.13	1.49	0.07		AA035834					

Table 1. Summary of protein properties and functions.

Msa.2851.0	1.00	-2.52	-4.32	2.71	-0.35	1.82	1.71	0.13	1.46	0.14	lipopolysaccharide binding protein; Lbp	X99347	lipopolysaccharide-binding protein precursor (lbp).	binds to the lipid moiety of bacterial lipopolysaccharides (lps), a glycolipid present in the outer membrane of all gram-negative bacteria. the lbp/lps complex seems to interact with the	2 83.0 cM		
Msa.117.0	1.00	-2.41	-1.85	0.94	-0.06	1.16	1.28	0.10	1.42	0.08	procollagen, type I, alpha 1; Col1a1	U08020	collagen alpha 1(i) chain precursor.	type i collagen is a member of group i collagen (fibrillar forming collagen).	11 56.0 cM	ECM (Matrix Prot)	
Msa.3557.0	1.00	-2.19	-2.73	1.67	-0.28	1.56	-0.45	0.87	1.40	0.19	stromal cell derived factor 3; Sdf3	W08269	pigment epithelium-derived factor precursor (pdf) (stromal cell-derived factor 3) (sdf-3).	neurotrophic protein; induces extensive neuronal differentiation in retinoblastoma cells. as it does not undergo the s (stressed) to r (relaxed) conformational transition characteristic of active serpins, it exhibits no serine protease		Cytokine	
L29454	1.00	-2.97	-2.34	0.83	-0.28	1.51	0.42	0.76	1.40	0.16	fibrillin 1; Fbn1	L29454	fibrillin 1 precursor.	structural component of connective tissue microfibrils that binds calcium. fibrillin-1-containing microfibrils provide long-term force bearing structural support	2 71.0 cM		
AA689977	1.00	-2.14	-0.71	1.22	0.22	1.67	1.16	1.17	1.38	0.10	mini chromosome maintenance deficient 6 (S. cerevisiae); Mcmd6	AA689977	dna replication licensing factor mcm6 (mis5 homolog).	may be involved in the control of a single round of dna replication during s phase. binds to chromatin during gl and detach from it during s phase as if it licenses the chromatin to replicate			

Table 1. Summary of the data for the fibronectin gene family.

M18194	1.00	-2.55	-1.79	0.59	0.17	1.34	0.50	0.78	1.36	0.09	fibronectin I; FnI	M18194	fibronectin precursor (fn) (fragments).	a glycoprotein that interacts with a variety of cells through both integrin and non-integrin receptors. encoded by a single gene, but alternative splicing of pre-mrna allows formation of multiple isoforms with critical roles in cell adhesion.	136.1 cM	Extracellular Protein	
AA285530	1.00	-2.38	-0.40	0.60	-1.07	0.02	0.66	0.94	1.35	0.14		AA285530					
Msa.10146.0	1.00	3.59	-1.35	1.51	0.33	2.24	1.37	0.24	1.31	0.14	vWF, human	AA168633				Hemostasis	
X56602	1.00	-7.23	-2.12	0.76	-5.94	0.81	-1.36	0.13	1.25	1.56	interferon-stimulated protein (15 kDa); Isg15	X56602	ubiquitin cross-reactive protein (interferon-stimulated protein 15).			Cytokine	
Msa.419.0	1.00	16.53	1.33	1.41	-1.51	0.36	-0.88	1.00	1.09	1.75	aminolevulinic acid synthase 2, erythroid; Alas2	M63244	5-aminolevulinic acid synthase, erythroid-specific, mitochondrial precursor (ec 2.3.1.37) (delta-aminolevulinate synthase) (delta-ala synthase) (alas2).	alas, though synthesized on cytoplasmic ribosomes, functions in mitochondria...alas2 encodes the erythrocyte-specific isoform involved in heme biosynthesis.	X 63.0 cM	Intracellular Protein	
U08020	1.00	-3.63	-2.35	1.03	0.52	2.00	1.42	0.36	1.07	0.81	procollagen, type I, alpha 1; Col1a1	U08020	collagen alpha 1(i) chain precursor.	type i collagen is a member of group i collagen (fibrillar forming collagen).	11 56.0 cM	ECM (Matrix Prot)	
AA289002	1.00	2.49	-0.24	0.54	-1.32	0.24	-0.42	1.25	1.03	0.69		AA289002				EST; Unknown	
AA684083	1.00	-0.55	0.43	0.57	-0.10	1.37	0.95	0.64	0.99	0.47		AA684083					
Msa.29141.0	1.00	-2.49	0.35	0.77	-0.06	1.40	0.94	1.18	0.96	0.67	myosin Ic; Myo1c	AA073795			11 44.13 cM		
Msa.17336.0	1.00	-2.35	0.72	0.79	0.14	1.33	0.88	1.00	0.94	0.70	melanoma X-actin; Actx	W89940		cells derived from the murine b16 melanoma express a third actin which has been designated melanoma x-actin. comparison between x-actin and i-actin structures indicate that x-actin is inherited by a different locus.		Structural Protein	
AA185262	1.00	2.41	-0.69	0.73	-0.01	1.41	1.73	1.87	0.89	0.79	EST; Unknown	AA185262				EST; Unknown	

Table 1. Summary of the results of the microarray analysis of the gene expression profile of the cells treated with anti-CD40L.

Msa.17592.0	1.00	-2.77	-0.35	0.83	-0.30	1.33	1.52	0.24	0.86	0.65		W96831							
Msa.29918.0	1.00	-2.55	0.41	1.16	-0.02	1.09	1.29	1.17	0.85	0.64	melanoma X-actin; Actx	AA087943							
AA396357	1.00	2.43	-2.33	2.31	0.23	1.34	0.26	0.80	0.71	0.59	ubiquitin-conjugating enzyme E2H; Ube2h	AA396357				66.5 cM			
U77460	1.00	1.01	-1.80	0.64	-0.72	2.22	3.58	0.80	0.70	0.59	complement component 3a receptor 1; C3ar1	U77460	c3a anaphylatoxin chemotactic receptor (c3a-r) component 3a receptor 1.	aka: anaphylatoxin c3a receptor, a g-protein coupled receptor	6 F1	Hemostasis			
Msa.4113.0	1.00	3.13	-1.07	2.02	0.00	2.06	-0.43	1.72	0.69	0.79	glucocorticoid-induced leucine zipper; Gilz	AA050733		expressed in normal lymphocytes from thymus, spleen, and lymph nodes, low or no expression detected in other nonlymphoid tissues, including brain, kidney, and liver. selectively protects t cells from apoptosis induced by treatment with anti-		Signal Transduction			
AA222661	1.00	-2.11	-0.06	0.66	-0.09	1.30	-0.44	1.04	0.64	0.61		AA222661							
AA530782	1.00	1.12	-4.81	4.02	-0.29	1.45	-1.23	1.08	0.58	1.24	keratin complex-1, gene C29; Krt1-c29	AA530782			11 57.85 cM				
AF033031	1.00	-0.44	0.93	0.44	0.13	1.15	1.66	1.07	0.56	0.69	solute carrier family 27 (fatty acid transporter), member 2; Slc27a2	AF033031	very-long-chain acyl coa synthetase (ec 6.2.1.-) (very-long-chain- fatty-acid-coa ligase).						
X03986	1.00	1.33	-5.21	1.97	-3.07	1.60	0.63	0.84	0.55	0.56	acetylcholine receptor alpha; Achr	X03986	acetylcholine receptor protein, alpha chain precursor.	the alpha, beta, gamma, and delta subunits of the muscle nicotinic acetylcholine receptor, each encoded by its own locus, are assembled into a pentamer of 2 alpha units and one each of the beta, gamma, and delta	243.0 cM	Receptor			
AA611341	1.00	1.31	-2.30	1.59	-0.58	5.09	-3.37	0.47	0.54	1.43	keratin complex-1, gene C29; Krt1-c29	AA611341			11 57.85 cM		EST; Unknown		
AA240803	1.00	4.90	0.13	0.59	-0.01	2.00	3.35	4.03	0.48	1.55	Unknown, No hits	AA240803						ECM (Matrix Prot)	
AB007848	1.00	-2.59	-1.24	0.53	0.22	1.88	-0.61	1.14	0.39	0.87	osteomodulin; Omd	AB007848		a novel bone matrix protein.					

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Table 1. Properties of plasminogen activators

Accession number	Gene name	Gene symbol	Gene description	Gene type	Gene location	Gene size (bp)	Gene length (aa)	Gene weight (kDa)	Gene pI	Gene isoelectric point (pI)	Gene molecular weight (kDa)	Gene function	Gene tissue	Gene expression	Gene regulation	Gene reference
AA426892	plasminogen activator, tissue; Plat	AA426892	plasminogen activator precursor (ec 3.4.21.68) (tpa) (t-pa) (t-plasminogen activator).	converts the abundant, but inactive, zymogen plasminogen to plasmin by hydrolyzing a single arg-val bond in plasminogen. by controlling plasmin-mediated proteolysis, it plays an important role in tissue remodeling and degradation, in cell migration and many other physiopathological	89.0 cM											
U16175	hypothetical protein, mucin 1, transmembrane, thrombospondin 3; LOC54129, Muc1, Thbs3	U16175	mucin 1 precursor (polymorphic epithelial mucin) (pemt) (episialin), thrombospondin 3 precursor.	a secreted glycoprotein member of the class of adhesive proteins. protein appears to have specialized functions in cell growth. thbs3 gene differs markedly from thbs1 and thbs2, both in structure and	3,342.6 cM,344.8 cM	Extracellular Protein										
X14194	nidogen 1; Nid1	X14194			13.7.0 cM											
Msa.18310.0	ATP citrate-lyase	AA000410		atp citrate-lyase is the primary enzyme responsible for the synthesis of cytosolic acetyl-coa in many tissues. strongly expressed in liver and adrenal, moderate levels were found in lung, brain, and large intestine. of importance in	Metabolic											

Table 1: Gene expression data for CD34 antigen

Msa.18226.0	1.00	-2.24	-1.41	1.06	-1.22	0.16	-0.69	0.92	-0.06	0.63	CD34 antigen	AA000252		possible adhesion molecule with a role in early hematopoiesis by mediating the attachment of stem cells to the bone marrow extracellular matrix or directly to stromal cells. could act as a scaffold for the attachment of	Cell Surface Protein	
W40995	1.00	1.18	-3.29	1.32	-1.94	0.73	-0.62	0.85	-0.07	0.70		W40995			EST; Unknown	
U19118	1.00	2.01	-0.96	0.81	-0.83	1.97	-1.82	0.18	-0.09	0.66	activating transcription factor 3; Atf3	U19118	cyclic-amp-dependent transcription factor atf-3 (activating transcription factor 3) (transcription factor lrg-21).	this protein binds the camp response element (cre) (consensus: 5'gtgacgt(a/c)(a/g)-3'), a sequence present in many viral and cellular promoters. represses transcription from promoters with atf sites. it may repress transcription by stabilizing the binding of inhibitory co-		
Msa.6450.0	1.00	-2.94	-2.22	1.18	-1.31	0.28	-1.43	0.25	-0.13	0.72	early quiescence protein-1; Eql	AA038318				
AA028265	1.00	-2.59	-1.71	1.05	0.65	2.25	-0.62	1.07	-0.13	1.09	fibromodulin	AA028265		fibromodulin, small collagen-binding proteoglycan of the extra-cellular matrix, mainly expressed in articular cartilage, tendon, ligament, leucine-rich repeat (lrr) family believed to function in the assembly of the collagen network in	ECM (Matrix Prot)	

Table 1

Msa.15338.0	1.00	2.11	-0.56	1.01	-0.01	1.28	-0.56	1.01	-0.13	0.74	glucocorticoid-induced leucine zipper; Gilz	AA097366		expressed in normal lymphocytes from thymus, spleen, and lymph nodes, low or no expression detected in other nonlymphoid tissues, including brain, kidney, and liver. selectively protects t cells from apoptosis induced by treatment with anti-CD3		Transcription Factor	
Msa.22717.0	1.00	1.99	-2.86	2.12	-0.02	1.43	-1.17	1.15	-0.17	0.99	actin alpha 3; Actn3	AA038082					
M22326-2	1.00	-1.55	-1.30	0.87	-2.26	0.11	-1.73	0.45	-0.29	0.85	early growth response protein 1; Egr1	M22326	early growth response protein 1 (egr-1) (krox-24 protein) (zif268).	transcriptional regulator. recognizes and binds to the dna sequence 5'-cgccccgc-3'(egr-site). activates the transcription of target genes whose products are required for mitogenesis and differentiation	18 16.0 cM	Intracellular Protein	
AA028499	1.00	1.67	-2.88	0.88	-0.48	1.69	-2.20	0.37	-0.32	1.28		AA028499					
Msa.5528.0	1.00	-2.83	-3.31	0.38	-3.53	2.03	-2.06	0.49	-0.44	0.97	retinol binding protein 4, plasma; Rbp4	W11638	plasma retinol-binding protein precursor (prbp) (rbp).	rbp delivers retinol from the liver stores to the peripheral tissues. in plasma, the rbp-retinol complex interacts with transthyretin, this prevents its loss by filtration through the kidney glomeruli	19 38.0 cM		
W35693	1.00	2.57	-1.92	0.93	-0.25	1.56	-0.30	0.98	-0.61	0.56	EST; Unknown	W35693				EST; Unknown	
Msa.2579.0	1.00	-2.09	-3.10	1.53	-0.55	1.69	-2.70	0.93	-0.63	0.78	DNA segment, human D4S114;	X70398		expressed in cns		Other	
AA048018	1.00	2.01	-1.54	0.61	0.10	1.39	-0.52	0.89	-0.70	0.69		AA048018					
Msa.2975.0	1.00	-2.13	-3.13	1.51	-0.57	1.76	-0.61	0.84	-0.71	0.66	retinol binding protein 4, plasma	W14367		plasma retinol binding protein (rbp4) and transthyretin complex with retinol to transport it from storage sites in the liver to target tissues. retinol modulates epithelial morphogenesis and epithelial differentiation		Extracellular Protein	

Table 1. Properties of myogenic factor 6; Myf6

X59060	1.00	1.85	-0.94	0.71	-0.32	1.40	4.80	1.20	-0.72	0.81	myogenic factor 6; Myf6	X59060	myogenic factor myf-6 (herculin).	myf6 or herculin is expressed in adult skeletal muscle, but not in smooth muscle, cardiac muscle, or non-muscular tissues. it activates expression of myod1 and myog. the level of expression of herculin is higher than for any of the other	10 59.0 cM	Transcription Factor	
Msa.15200	1.00	-3.48	-3.48	2.00	-1.38	0.16	-1.75	0.30	-0.72	0.58	CD34 antigen	W65699		possible adhesion molecule with a role in early hematopoiesis by mediating the attachment of stem cells to the bone marrow extracellular matrix or directly to stromal cells. could act as a scaffold for the attachment of		Cell Surface Protein	
AA530179	1.00	1.05	-3.59	2.01	-0.08	2.05	-3.74	0.67	-0.74	1.69	S100 calcium binding protein A3; S100a3	AA530179	s100 calcium-binding protein a3 (s-100e protein).	binds both calcium and zinc. probably binds 2 zinc ions per molecule (by	3 43.6 cM		
Msa.7352.0	1.00	1.81	-2.64	0.53	-0.82	2.09	-0.65	0.85	-0.76	0.70		AA008667					
AA562685	1.00	-1.16	-2.39	0.61	-0.55	2.04	-0.95	1.17	-0.79	0.84	procollagen, type I, alpha 1	AA562685		type i collagen is of particular importance in the extracellular matrix of bone, skin, tendon, and dentine, and is highly expressed in fibroblasts. it is known to be expressed in mouse palatal shelves		ECM (Matrix Prot)	
Msa.723.0	1.00	-2.06	-2.76	1.29	-1.31	0.12	-0.57	0.81	-0.82	0.62	aquaporin 1; Aqp1	L02914	aquaporin-chip (water channel protein for red blood cells and kidney proximal tubule) (aquaporin 1) (early response protein der2)	forms a water-specific channel that provides the plasma membranes of red cells and kidney proximal tubules with high permeability to water	6 27.0 cM	Cell Surface Protein	
Msa.17890.0	1.00	1.98	-3.38	2.16	-0.23	1.33	-1.21	0.05	-0.86	0.69	eukaryotic translation elongation factor 2; Eef2	W98531					

Table 1. Properties of keratins and their associated proteins.

K02108	1.00	2.14	-0.92	1.29	0.82	1.99	0.19	1.31	-0.86	0.84	keratin complex 2, gene 6a; Krt2-6a	K02108	keratin, type ii cytoskeletal 6 (cytokeratin 6) (ck6) (k6 keratin).	there are two types of cytoskeletal and microfibrillar keratin: i (acidic; 4-55 kda) [k9 to k2] and ii (neutral to basic; 56-7 kda) [k1 to k8]. both a basic and an acidic keratin are required for filament assembly.	15		
AA185284	1.00	2.23	-2.22	0.43	-0.83	1.88	-1.32	0.14	-0.86	0.64		AA185284					
W41417	1.00	3.44	-2.19	1.11	-0.36	1.43	-1.53	0.23	-0.94	0.83		W41417					
Msa.1170.0	1.00	1.37	-3.82	2.50	0.06	2.16	-2.69	0.44	-0.98	1.39	keratin-associated protein 5-1; Krtap5-1	M37759		keratin-associated protein 5-1		Other	
W81858	1.00	1.23	-2.53	0.85	-0.68	1.89	-1.81	1.47	-1.07	0.94	kinesin light chain 1; Klc1	W81858			12 57.0 cM		
C77823	1.00	1.13	-1.83	0.58	-0.57	2.16	-0.67	1.04	-1.08	0.83		C77823					
AF020194	1.00	1.05	-3.83	2.27	-0.41	1.77	-1.05	1.19	-1.08	0.80	taurine/beta-alanine transporter; Taut	AF020194	sodium- and chloride-dependent taurine and beta-alanine transporter.	an amino acid transporter, found primarily in brain.	6 38.2 cM	Cell Surface Protein	
Msa.43191.0	1.00	1.18	-3.36	0.99	-1.28	2.65	-0.86	1.24	-1.09	0.96	integrin-associated protein; Itgp	Z25524				Cell Surface Protein	
X63023	1.00	2.54	0.34	0.51	0.25	1.30	-1.13	0.04	-1.14	0.03	cytochrome P450, steroid inducible 3a13; Cyp3a13	X63023	cytochrome p450 3a13 (ec 1.14.14.1) (cyp3a13).	can activate aflatoxin b1 to a genotoxic product.	5		
Msa.22263.0	1.00	-2.02	-1.25	1.32	-0.12	1.28	-0.50	0.92	-1.17	0.11		AA033333					
C80656	1.00	1.58	-3.32	1.44	-0.59	1.91	-0.79	2.01	-1.20	0.87	Unknown	C80656				EST; Unknown	
Msa.1531.0	1.00	1.97	-2.54	1.23	-1.29	0.24	-0.65	0.88	-1.21	0.07	apolipoprotein D; Apod	L39123	apolipoprotein d precursor.	apod occurs in the macromolecular complex with lecithin-cholesterol acyltransferase. it is probably involved in the transport and binding of bilin. appears to be able to transport a variety of ligands in a number of different contexts.	16 21.2 cM	Extracellular Protein	
Msa.9372.0	1.00	1.75	-2.72	1.03	-1.67	0.58	-2.02	0.43	-1.22	0.76	CD59 antigen; Cd59	W41339			2 55.0 cM		

Msa.383.0	1.00	2.36	-1.59	2.09	-0.22	1.48	-1.20	0.07	-1.28	0.12	erythrocyte protein band 4.1; Epb4.1	L00919	protein 4.1 (band 4.1) (p4.1).	protein 4.1 is a major structural element of the erythrocyte membrane skeleton. it plays a key role in regulating membrane physical properties of mechanical stability and deformability by stabilizing spectrin-actin interaction. binds with a high affinity to glycophorin and with lower affinity to band 4.1.	4 65.7 cM	Intracellular Protein
X82648	1.00	2.15	-1.74	0.84	-1.17	0.14	-0.69	0.88	-1.32	0.08	apolipoprotein D; Apod	X82648	apolipoprotein d precursor.	apod occurs in the macromolecular complex with lecithin-transport and binding of bilin. appears to be able to transport a variety of ligands in a number of different contexts	16 21.2 cM	Other
Msa.5789.0	1.00	1.98	-3.40	2.07	-0.23	1.46	-0.65	1.07	-1.34	0.16		W18503				
AA673431	1.00	-2.43	-0.84	0.75	0.23	1.52	0.71	1.09	-1.35	0.19		AA673431				EST; Unknown
Msa.5254.0	1.00	-2.55	-2.67	1.27	-1.48	0.08	-1.88	0.35	-1.43	0.13		AA064307				
Msa.21971.0	1.00	1.10	-4.46	1.91	-1.55	2.64	-0.54	1.03	-1.44	0.12		AA154451				
Msa.14179.0	1.00	2.98	-2.90	1.25	-0.15	1.67	-0.92	1.23	-1.47	0.96	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34 kDa), member 17; Slc25a17	AA118682				
AA162560	1.00	1.07	-2.54	0.34	-2.59	0.16	-1.60	0.16	-1.47	0.15		AA162560				
X57024	1.00	1.10	-4.45	2.19	-1.76	0.36	-1.55	0.25	-1.48	0.18	glutamate dehydrogenase; Glud	X57024	glutamate dehydrogenase precursor (ec 1.4.1.3) (gdh).		14 15.5 cM	Metabolic
AA198316	1.00	2.64	-0.11	0.83	1.38	0.08	0.33	1.10	-1.51	0.18	acyl-CoA thioesterase 1, cytosolic; Ctel-1, pending	AA198316			12	

Table 1

Msa.2414.0	1.00	1.72	-2.35	1.26	-0.70	0.64	-1.30	0.17	-1.53	0.19	laminin, alpha 3; Lama3	X84014	laminin alpha-3 chain precursor (fragment).	laminin-5 is thought to be involved in (1) cell adhesion via integrin alpha-3/beta-1 in focal adhesion and integrin alpha-6/beta-4 in hemidesmosomes, (2) signal transduction via tyrosine phosphorylation of pp125-fak and p8, (3) differentiation of keratinocytes (by	18 3.0 cM		
AA237919	1.00	-0.03	-2.41	0.90	-0.29	1.68	-1.58	0.35	-1.53	0.46		AA237919					
AA028657	1.00	1.12	-2.28	0.70	-0.54	1.87	-2.01	0.46	-1.60	1.03	EST; Unknown	AA028657				EST; Unknown	
Msa.330.0	1.00	1.53	-5.88	2.92	-2.03	0.91	-1.61	0.39	-1.63	0.36	upstream transcription factor 2; Usf2	U12283	upstream stimulatory factor 2 (upstream transcription factor 2) (major late transcription factor 2).	bhlh protein that is ubiquitously expressed. transcription factor that binds to e-boxes (5'-cacgtg-3') found in a variety of viral and cellular promoters. forms bhlh dimers for dna binding. binds dna as homodimer or heterodimer (see also U12283).	7 11.0 cM	Transcription Factor	
Msa.40899.0	1.00	1.40	-2.51	0.86	-1.22	0.17	-3.58	0.96	-1.64	1.30	EST to MYH8	AA162395		m36769 homo sapiens perinatal myosin heavy chain 8% to human			
Msa.42549.0	1.00	-2.37	-0.31	1.04	-0.14	1.77	-1.06	1.30	-1.65	0.27	est	AA168690		similar to calmodulin		EST; Unknown	
AA266377	1.00	2.21	-1.86	0.25	-1.53	0.40	-1.67	0.31	-1.69	0.22		AA266377	platelet-endothelial tetraspan antigen 3 (peta-3) (gp27) (membrane glycoprotein sfa-1) (cd151 antigen).				
Msa.8112.0	1.00	-2.17	-2.20	0.84	-0.38	1.57	-0.54	0.89	-1.71	0.97	CD151 antigen; Cd151	AA050218			7 23.5 cM		
D17577	1.00	-2.15	-0.33	0.69	1.25	0.06	-1.82	0.43	-1.72	0.24	kinesin heavy chain member 1B; Kif1b	D17577	kinesin-like protein kif1b.	kif1b works as a monomeric motor for anterograde transport of mitochondria.	4 70.9 cM	Structural Protein	

Table 1. Amino acid composition of the protein

Msa.2160.0	1.00	1.96	-6.25	5.84	-0.10	1.23	-1.32	0.08	-1.72	0.13	apolipoprotein CI; ApocI	AA049273	apolipoprotein c-i precursor (apo-ci).	low molecular weight surface components of chylomicrons and of very low density (vldl) and high density (hdl) lipoproteins. functions may include activation of lecithin:cholesterol acyltransferase, and inhibition of apoc binding to the hdl receptor	7 4.0 cM	Other	
U37222	1.00	-2.07	-1.65	0.64	-1.51	0.04	-3.13	1.34	-1.73	0.14	adipocyte complement related protein of 30 kDa; Acrp30	U37222	30 kda adipocyte complement-related protein precursor (acrp30) (adipocyte specific protein adipon)	may function as a signaling molecule for adipose tissue.			
AA237797	1.00	1.15	-2.54	0.76	-0.57	1.88	-2.14	0.54	-1.75	1.03	EST; Unknown	AA237797				EST; Unknown	
Msa.33047.0	1.00	-2.09	-1.89	0.98	0.71	0.91	1.19	0.14	-1.76	1.51	CD151 antigen; Cd151	AA109912	platelet-endothelial tetraspan antigen 3 (peta-3) (gp27) (membrane glycoprotein sfa-1) (cd151 antigen).	gene expression was observed in many cell types, but was either absent or present at a low level in brain and lymphoid cells and tissues, including thymus and spleen. contains four putative transmembrane domains, a number of	7 23.5 cM	Cell Surface Protein	
Msa.370.0	1.00	1.28	-2.88	0.74	-1.69	0.28	-1.62	0.39	-1.79	0.35	peroxisomal membrane protein 3, 35 kDa; Pxmp3	L27842	peroxisome assembly factor-1 (paf-1) (peroxin-2).	somehow implicated in the biogenesis of peroxisomes.			
Msa.13629.0	1.00	1.77	-5.94	4.06	-1.56	0.40	-1.67	0.26	-1.80	0.36		AA155371					
Msa.43204.0	1.00	1.11	-1.96	0.42	-1.63	0.42	-2.18	0.61	-1.85	0.83	serine protease inhibitor 1-1; Spi1-1	M75721	alpha-1-antitrypsin 1-1 precursor (serine protease inhibitor 1-1) (alpha-1 protease inhibitor 1) (alpha-1-	inhibitor of serine proteases. its primary target is elastase, but it also has a moderate affinity for plasmin and thrombin.	12 51.0 cM		
D30782	1.00	2.46	-0.98	0.66	-1.36	0.17	-2.84	0.63	-1.85	0.18	epiregulin; Ereg	D30782					
W97690	1.00	1.87	-3.28	1.59	-1.46	0.19	-1.78	0.22	-1.97	0.28		W97690					
Msa.40750.0	1.00	1.20	-2.95	0.51	-1.94	0.71	-1.81	0.34	-2.05	0.38	polypyrimidine tract binding protein 2; Ptb2-pending	AA155318					
AF030001E NETNX	1.00	-2.22	-2.62	1.21	-0.40	1.83	-2.62	0.67	-2.06	2.03	Cosmid sequence (>200K)	AF030001				EST; Unknown	

Table 1: "Cellular Data"

U30840	1.00	1.36	-1.71	0.55	-1.49	0.32	-1.88	0.17	-2.25	0.09	voltage-dependent anion channel 1; Vdac1	U30840	voltage-dependent anion-selective channel protein 1 (mvdac1) (outer mitochondrial membrane protein porin 1).	forms a channel through the mitochondrial outer membrane that allows diffusion of small hydrophilic molecules. the channel adopts an open conformation at low or zero membrane potential and a closed conformation at potentials above 3-4 mv. the open state has a weak anion selectivity whereas the closed state is cation-	11 29.0 cM		
J03398	1.00	-1.60	-2.11	0.74	-1.32	0.07	-4.66	0.85	-2.29	1.31	P glycoprotein 2; Pgy2	J03398	multidrug resistance protein 2 (p-glycoprotein 2).	mdr gene encoding a multidrug resistance protein mma	5 1.0 cM	Cell Surface Protein	
X61433	1.00	1.06	-1.90	0.33	-1.48	0.10	-2.09	0.36	-2.30	0.12	ATPase, Na+/K+ transporting, beta 1 polypeptide; Atp1b1	X61433	sodium/potassium-transporting atpase beta-1 chain (sodium/potassium-dependent atpase beta-1 subunit).	expressed in brain, kidney, lung, testis, and heart. not found in the liver. expression occurs in pre-b lymphocytes, resting b cells in the bone marrow, pre-t cells, and mature thymocytes. mitogen-stimulated t and b cells.	1 86.8 cM	Cell Surface Protein	
Msa.2879.0	1.00	1.32	-2.74	1.40	-1.53	0.12	-2.62	0.14	-2.31	0.27	transducer of ErbB-2.1; Tob1	D78382	tob protein (transducer of erb-2).	anti-proliferative protein that interacts with the erb-2 receptor tyrosine kinase. may physically and/or functionally interact with protein-tyrosine kinase receptors (by similarity)			

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X06115	1.00	1.44	-1.93	0.73	-1.54	0.07	-1.83	0.07	-2.31	0.24	cadherin 1; Cdh1	X06115	epithelial-cadherin precursor (e-cadherin) (uvomorulin) (arc-1).	cadherins are calcium dependent cell adhesion proteins. they preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell	8 53.3 cM		
Msa.3250.0	1.00	1.14	-4.21	2.32	-1.75	0.48	-1.66	0.34	-2.32	0.40	histidyl tRNA synthetase; Hars	U39473	histidyl-tma synthetase (ec 6.1.1.21) (histidine--tma ligase) (hists).				
Msa.29324.0	1.00	1.63	-1.48	1.37	-1.32	0.26	-2.00	0.18	-2.33	0.11		AA080197					
Msa.4067.0	1.00	1.73	-2.15	0.61	-0.72	1.74	-0.78	1.03	-2.34	0.57	Sip1?	AA003876		splicing factor (homo sapiens)		Unknown	
Msa.5481.0	1.00	1.28	-2.81	1.61	-1.56	0.02	-2.00	0.09	-2.35	0.13	annexin A8; Anxa8	AA060106			14 13.0 cM	EST; Unknown	
AB000713	1.00	-0.50	-1.12	1.24	1.23	0.05	-1.86	0.34	-2.35	0.72	claudin 4; Cldn4	AB000713	claudin-4 (clostridium perfringens enterotoxin receptor) (cpe-receptor) (cne-r).	a 4 transmembrane domain protein that is a novel component of tight junction strands of liver and kidney.	5 75.0 cM	Cell Surface Protein	
AA615066	1.00	2.07	-4.34	2.32	-0.57	1.61	-1.58	0.35	-2.38	0.54		AA615066					
Msa.39064.0	1.00	1.13	-2.50	1.11	-1.58	0.22	-2.58	0.28	-2.39	0.18	titin (series elastic element of striated muscle)	AA145312		titin, giant sarcomeric protein, extending from the m line to the z line of striated muscle sarcomere, essential in the temporal and spatial control of the assembly of the highly ordered sarcomeres of striated muscles.		Structural Protein	

Table 1. Properties of gap junction proteins and associated proteins.

Msa.570.0	1.00	1.28	-3.02	2.47	-0.25	1.42	-2.54	0.82	-2.43	0.44	gap junction membrane channel protein beta 2; Gjb2	M81445	gap junction beta-2 protein (connexin 26) (cx26).	one gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell	14 21.0 cM		
C77662	1.00	1.30	-2.44	0.87	-1.40	0.22	-2.48	0.29	-2.44	0.36		C77662					
Msa.3940.0	1.00	-1.09	-2.21	0.57	-1.72	0.18	-2.20	0.33	-2.44	0.12	Rev-ErbA-alpha protein; rat	W13191		most similar in structure to the thyroid hormone receptor (c-erba) and the retinoic acid receptor, but it does not bind either thyroid hormone or retinoic acid. the mma encoding rev-erba alpha is present in many tissues and is particularly a		Receptor	
AA690434	1.00	1.12	-1.86	0.32	-1.84	0.50	-2.52	0.38	-2.45	0.11		AA690434					
M72414	1.00	1.68	-4.09	1.85	-2.21	0.09	-2.62	0.48	-2.47	0.24	microtubule-associated protein 4; Mtap4	M72414	microtubule-associated protein 4.	non-neuronal microtubule-associated protein. promotes microtubule	9 58.0 cM		
Msa.799.0	1.00	-1.57	-3.69	1.19	-2.69	0.73	-2.24	0.25	-2.48	0.30	interferon-related developmental regulator 1; Ifrd1	J00424	interferon-related developmental regulator 1 (nerve growth factor-inducible protein pc4) (tpa induced sequence 7) (tis7 protein).	could play a role in regulating gene activity in the proliferative and/or differentiative pathways induced by ngf. may be an autocrine factor that attenuates or amplifies the initial ligand		Cytokine	
W29651	1.00	1.11	-4.23	2.14	-1.98	0.01	-2.48	0.34	-2.48	0.30		W29651					
AA688835	1.00	-1.76	-3.43	1.28	-1.97	0.08	-2.48	0.61	-2.51	0.10	Unknown	AA688835				EST; Unknown	
AJ001118	1.00	1.17	-2.97	0.97	-2.10	0.28	-2.89	0.25	-2.56	0.14	monoglyceride lipase; MglI	AJ001118			3		
Msa.19265.0	1.00	2.33	-2.61	0.87	-1.88	0.75	-1.96	0.52	-2.57	0.53	golgi autoantigen, golgin subfamily a, 4; Golga4	AA009086					
AF026489	1.00	1.67	-2.26	0.77	-1.75	0.32	-2.22	0.24	-2.62	0.19	beta-spectrin 3; Spnb3	AF026489			19 0.0 cM		
Msa.28719.0	1.00	1.54	-3.87	1.00	-3.39	1.49	-2.22	0.10	-2.65	0.05		AA072611					

Msa.9757.0	1.00	1.17	-7.61	6.54	-1.66	0.42	-2.17	0.25	-2.67	0.19	basic transcription element binding protein 2; Klf5	AA014295					
X97986	1.00	1.11	-1.97	1.84	-1.42	0.40	-3.01	1.27	-2.71	0.34	desmocollin 1; Dsc1	X97986	desmocollin 1a/1b precursor.	component of intercellular desmosome junctions. involved in the interaction of plaque proteins and intermediate filaments mediating cell-cell adhesion. may contribute to epidermal cell positioning (stratification) by mediating differential adhesiveness between cells that express different isoforms. linked to the			
Msa.32581.0	1.00	1.41	-2.38	1.08	-1.25	0.21	-2.58	0.43	-2.72	0.11	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4; Slc25a4	AA107658	adp.atp carrier protein, heart/skeletal muscle isoform t1 (adp/ATP translocase 1) (adenine nucleotide translocator 1) (ant	carries adenosine triphosphate (ATP) from the mitochondrial matrix into the intermembrane space and the diphosphate (ADP) in the reverse	8 26.0 cM	Other	
Msa.450.0	1.00	-1.56	-3.38	1.69	-1.73	0.11	-4.22	2.40	-2.74	0.20	adipsin; Adn	W36455	d precursor (ec 3.4.21.46) (c3 convertase activator) (properdin factor d) (adipsin) (28 kDa protein, adipocytel)	a serine protease synthesized principally in adipose tissue, but also by sciatic nerve... adipsin is suppressed (more than 1-fold) in genetically obese mice	10 43.0 cM	Proteolytic	
Msa.11196.0	1.00	1.31	-1.76	0.72	-1.74	0.44	-1.70	0.37	-2.74	0.24		W50088					
U06670	1.00	1.16	-2.84	1.03	-1.65	0.01	-3.54	1.46	-2.75	0.44	very low density lipoprotein receptor; Vldlr	U06670	very low-density lipoprotein receptor precursor (vldl receptor).	binds vldl and transports it into cells by endocytosis. in order to be internalized, the receptor-ligand complexes must first cluster into clathrin-coated pits	19 20.0 cM	Receptor	

Msa.23977.0	1.00	1.39	-2.52	1.29	-1.22	0.04	-2.57	0.68	-2.76	0.26	EST	W07946		geneseqn:z9721 human secreted protein gene 3 cdna clone hwhgu54, seq id no:13. new isolated human genes and the secreted treatment of e.g. cancers			
W71831	1.00	1.37	-5.51	3.22	-1.70	0.18	-3.58	1.40	-2.76	0.36	histone deacetylase 5; Hdac5	W71831					
U12785	1.00	1.04	-2.41	0.64	-1.96	0.28	-2.62	0.39	-2.77	0.07	alcohol dehydrogenase family 3, subfamily A1; Aldh3a1	U12785	aldehyde dehydrogenase, dimeric nadp-preferring (ec 1.2.1.5) (aldh class 3) (dioxin-inducible aldehyde dehydrogenase-3); fatty aldehyde dehydrogenase (ec 1.2.1.3) (aldehyde dehydrogenase, microsomal) (aldh class 3).	aldhs play a major role in the detoxification of alcohol-derived acetaldehyde. they are involved in the metabolism of corticosteroids, biogenic amines, neurotransmitters, and lipid peroxidation. this protein preferentially oxidizes aromatic aldehyde substrates. it may play a role in the oxidation of toxic	11 34.25		
AA462409	1.00	1.14	-1.61	1.30	-1.49	0.25	-2.23	0.31	-2.81	0.04	Unknown	AA462409				EST;	
Msa.4575.0	1.00	-1.01	-2.05	1.68	-1.47	0.36	-2.53	0.73	-2.81	0.20	EST	AA065868		geneseqn:z56885 human sbpsapl polypeptide encoding est derived sequence. new polypeptides of prosaposin family, antagonist and inhibitors for treatment			
Msa.16748.0	1.00	2.17	-2.91	1.31	-1.55	0.39	-2.81	0.81	-2.83	0.59		W78443					
Msa.3237.0	1.00	1.01	-2.22	1.69	-1.64	0.57	-1.49	0.07	-2.83	0.29	four and a half LIM domains 1; Fhl1	W14830		fhl1 and fhl3 were expressed in a number of skeletal muscles while fhl2 was expressed at high levels in cardiac muscle. may have an involvement in muscle development or	X A6-A7.1	Regulatory	

Table 1: "Fatty acid"

AA028770	1.00	0.02	-2.96	1.22	-0.34	1.56	-2.74	0.63	-2.86	1.02	Cysteine Rich protein 2, rat	AA028770		expressed in differentiated vascular smooth muscle cells. during development crp2/smlim expression decreased in the heart but remained high in the vasculature		Regulatory	
M91236	1.00	1.28	-2.27	1.21	-1.61	0.53	-2.93	1.20	-2.86	0.27	gap junction membrane channel protein beta 5; Gjb5	M91236	gap junction beta-5 protein (connexin 30.3) (cx30.3).	one gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell	4 57.5 cM		
W62701	1.00	1.71	-3.09	2.19	-0.68	0.74	-2.36	0.14	-2.88	0.52		W62701					
Msa.6594.0	1.00	1.58	-1.24	1.11	-0.37	1.53	-4.56	2.63	-2.92	0.36		W30612					
Msa.7275.0	1.00	1.19	-1.82	1.28	-1.28	0.03	-2.67	0.32	-2.95	0.31	Mus musculus phosphofructokinase-1 A isozyme (PFka)	W17917					
Msa.26512.0	1.00	1.31	-1.53	1.17	-1.38	0.29	-2.28	0.39	-3.01	0.48	tubulin alpha 8; Tuba8	AA063914					
X13135	1.00	1.12	-4.53	1.73	-2.16	0.14	-3.08	0.44	-3.06	0.45	fatty acid synthase; Fasn	X13135	fatty acid synthase (ec 2.3.1.85) [includes: ec 2.3.1.38; ec 2.3.1.39; ec 2.3.1.41; ec 1.1.1.100; ec 4.2.1.61; ec 1.3.1.10; ec	fatty acid synthase (fas) catalyzes the last step in the fatty acid biosynthetic pathway.	11 72.0 cM	Metabolic	
Msa.3669.0	1.00	-1.55	-1.69	0.98	-1.64	0.34	-2.26	0.62	-3.06	0.28	est	W08486				EST; Unknown	
AA138388	1.00	1.25	-2.10	0.49	-1.90	0.24	-1.97	0.25	-3.07	0.63		AA138388					
U62295	1.00	1.09	-3.22	1.18	-1.83	0.38	-2.99	0.47	-3.07	0.10	cytochrome P450, 2j6; Cyp2j6	U62295	cytochrome p450 2j6 (ec 1.14.14.1) (cyp1j6) (arachidonic acid epooxygenase).		4 46.5 cM		
Msa.2753.0	1.00	-1.18	-5.10	2.45	-1.92	0.61	-2.80	0.31	-3.08	0.53	laminin, beta 2; Lamb2	U43541	laminin beta-2 chain precursor.	extracellular matrix glycoproteins which are major components of basement membranes	9 60.0 cM	ECM (Matrix Prot)	
AA734300	1.00	1.09	-2.42	0.84	-1.93	0.62	-2.71	0.59	-3.10	0.48	Hypothetical protein FLJ20171; human	AA734300				Unknown	

Table 1. Amino acid sequence of myosin heavy chain, embryonic (fragment).

Msa.30092.0	1.00	1.23	-8.99	6.81	-1.44	0.05	-5.46	1.82	-3.29	0.54	myosin, heavy polypeptide 3, skeletal muscle, embryonic: Mvh3 EST to LTBp4	AA089202	myosin heavy chain, fast skeletal muscle, embryonic (fragment).	muscle contraction.	11 35.0 cM		
Msa.23986.0	1.00	-1.13	-2.92	0.87	-1.80	0.13	-3.03	0.46	-3.30	0.65		W16389		latent transforming growth factor 6% nucleotide level			
AA423082	1.00	1.23	-2.92	0.98	-1.73	0.72	-2.72	0.71	-3.37	0.72	Unknown	AA423082				EST; Unknown	
Msa.21797.0	1.00	1.31	-2.77	0.75	-1.85	0.02	-3.30	0.31	-3.44	0.32	ADP-ribosyltransferase 3 (Art3)	AA028701				Other	
Msa.1286.0	1.00	1.60	-3.15	1.51	-2.15	0.66	-6.37	2.47	-3.45	1.64	wingless-related MMTV integration site 4; Wnt4	M89797	wnt-4 protein precursor.	may be an intracellular signaling molecule involved in segmentation of the forebrain. is likely to signal over only few cell diameters (by similarity). seems to be involved in kidney development	14		
X51829	1.00	1.04	-4.58	2.18	-2.40	0.50	-2.90	0.28	-3.48	0.39	myeloid differentiation primary response gene 116; Mvd116	X51829	myeloid differentiation primary response protein mvd116.			Other	
Msa.3168.0	1.00	1.09	-3.46	1.73	-1.64	0.00	-2.65	0.18	-3.66	0.88	gap junction membrane channel protein beta 6; Gjb6	Z70023	gap junction beta-6 protein (connexin 30) (cx30).	one gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell	14		
ET62740	1.00	2.18	-2.68	0.86	-2.03	0.73	-2.43	0.60	-3.69	0.95	ankyrin 3, epithelial; Ank3	ET62740			10 38.0 cM		
M74495	1.00	-1.28	-1.86	1.37	-1.22	0.02	-2.60	0.64	-3.70	0.25	adenylosuccinate synthetase 1, muscle; Adss1	M74495	adenylosuccinate synthetase, muscle isozyme (ec 6.3.4.4) (imp-- aspartate ligase) (adss) (amnsase)	plays an important role in the de novo pathway of purine nucleotide biosynthesis.			
AA407234	1.00	1.93	-2.78	0.47	-2.39	1.02	-3.71	1.15	-3.74	0.79		AA407234					

U76618	1.00	1.16	-1.51	1.02	-1.52	0.24	-1.60	0.21	-3.77	0.45	nebulin-related anchoring protein; Nrap	U76618	specific to skeletal and cardiac muscle, not detected by northern blot in non-muscle. localized at myotendinous junction in mouse skeletal muscle and intercalated disc in cardiac muscle. plays a role in anchoring	19 53.25 cM	Structural Protein	
AA717225	1.00	-1.07	-2.01	0.52	-1.49	0.03	-2.85	0.77	-3.80	0.63		AA717225				
Msa.15880.0	1.00	-5.84	-2.18	1.33	-1.49	0.24	-2.09	0.30	-3.81	0.73	neuropeptide Y, NPY	W70782	implicated in the control of feeding and in secretion of gonadotrophin-release hormone.		Other	
M81086	1.00	1.11	-2.08	0.96	-1.62	0.39	-5.80	3.35	-3.82	0.31	tropomyosin 2, beta; Tpm2	M81086	an actin-associated cytoskeletal protein. different isoforms occur in skeletal muscle and in smooth muscle and nonmuscle cells		Structural Protein	
AF026072	1.00	-0.16	-1.09	1.73	-0.29	1.69	-2.40	1.47	-3.83	1.01	hydroxysteroid sulfotransferase; SULT2B	AF026072				
C80836	1.00	1.45	-3.34	1.10	-2.41	0.17	-6.22	1.90	-3.83	1.08	EST; unknown	C80836			EST; Unknown	
AA265119	1.00	-2.16	-2.71	0.67	-2.32	0.55	-6.91	3.49	-3.90	0.53	EST; Unknown	AA265119			EST; Unknown	
D42048	1.00	-1.41	-1.83	1.36	-1.80	0.64	-2.87	0.48	-3.92	0.40	squalene epoxidase; Sqle	D42048	squalene monooxygenase (cc 1.14.99.7) (squalene epoxidase) (se).			
Msa.400.0	1.00	1.24	-4.47	1.71	-2.24	0.01	-4.10	0.65	-3.98	0.71	myosin heavy chain, cardiac muscle, adult; Myhca	M76601	myosin heavy chain, cardiac muscle alpha isoform.	14 20.0 cM	Structural Protein	
U76371	1.00	1.17	-1.64	1.11	-0.08	1.23	-4.77	1.17	-4.01	1.08	CD8beta opposite strand; Bop	U76371	a transcribed gene designated as bop, is a cd8-beta opposite direction transcript. detected in mouse thymus only, and may be limited to cd8+ t cells	6 30.5 cM	Other	

Msa.5248.0	1.00	1.53	-3.03	1.51	-1.52	0.11	-3.41	0.56	-4.02	0.44	phosphofructokinase-1 A isozyme (PfkA)	W11082		defects in pfkm are the cause of glycogen storage disease viii (gsd-vii) (also known as tarui's disease); a disease characterized by exercise intolerance with associated nausea and vomiting		Metabolic		
U15541	1.00	1.39	-1.98	1.01	-1.30	0.23	-3.58	1.33	-4.05	0.43	cytochrome c oxidase, subunit VIIIb; Cox8b	U15541	cytochrome c oxidase polypeptide viii-heart precursor (ec 1.9.3.1).	this protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport	7 68.8 cM	Metabolic		
Msa.1716.0	1.00	1.52	-2.53	1.21	-1.25	0.14	-3.16	0.63	-4.17	0.61	cytochrome c oxidase, subunit VIIIb; Cox8b	AA028501	cytochrome c oxidase polypeptide viii-heart precursor (ec 1.9.3.1).	this protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport	7 68.8 cM	Metabolic		
Msa.26364.0	1.00	-1.67	-2.77	1.15	-1.53	0.32	-4.00	0.27	-4.18	0.77	mmDNAJA4	AA062328		murine cdna encoding a novel type i hsp4/dnaj homolog, mmdja4(1) biochim. biophys. acta 1493 (1996) 1-10		Regulatory		
Msa.27761.0	1.00	1.08	-6.28	3.32	-2.67	0.08	-2.84	0.35	-4.39	0.45	ethanol induced 6; Etol6	AA068578						
X61600	1.00	1.16	-2.57	1.60	-1.20	0.04	-11.98	5.36	-4.41	1.00	enolase 3, beta muscle; Eno3	X61600	beta enolase (ec 4.2.1.11) (2-phospho-d-glycerate hydro-lyase) (skeletal muscle enolase)		11 42.0 cM	Metabolic		
AA688542	1.00	1.29	-4.38	2.50	-1.47	0.07	-2.37	0.31	-4.49	0.53	N-myc downstream regulated 2; Ndr2	AA688542	ndrg2 protein (ndr2 protein).					
Msa.2491.0	1.00	-2.38	-6.72	3.49	-2.04	0.41	-3.15	0.11	-4.58	0.59	tenascin X; Tnx	X73959		extracellular matrix glycoproteins probably of importance in regulating developmental processes	17 18.74	ECM (Matrix Prot)		
AA033394	1.00	1.52	-3.15	1.22	-1.53	0.19	-5.64	1.78	-4.61	0.82	muscle glycogen phosphorylase; Pygm	AA033394			19 2.0 cM	Metabolic		
X67141	1.00	1.04	-3.72	1.84	-0.79	0.74	-7.20	3.32	-4.63	1.28	parvalbumin; Pva	X67141	parvalbumin alpha.	in muscle, the calcium-binding protein parvalbumin is thought to be involved in muscle relaxation.	15 45.7 cM	Extracellular Protein		

Table 1. Properties of the proteins of the desmosomes and adherens junctions.

Msa.13213.0	1.00	1.37	-5.96	3.66	-1.84	0.19	-5.66	0.99	-5.68	0.86	actinin alpha 2; Actn2	W53582			13 7.0 cM	Structural Protein	
Msa.2776.0	1.00	1.32	-3.40	1.87	-1.41	0.24	-2.27	0.48	-6.03	1.83	junction plakoglobin; Jup	M90365	junction plakoglobin (desmoplakin iii) (fragment).	one of the proteins of desmosomal membrane anchorage site plaques of the epithelium, and is also a component of plaques of the adherens junction	11 60.0 cM	Structural Protein	
AA562768	1.00	2.21	-7.37	1.45	-3.74	2.31	-7.62	2.96	-6.40	1.95	glioblastoma amplified sequence; Gbas	AA562768				Other	
Msa.2946.0	1.00	1.13	-4.57	1.95	-2.15	0.90	-2.87	0.34	-6.70	0.89	cysteine-rich protein 3; Crp3	W08774	ccaat/enhancer binding protein delta (c/ebp delta) (c/ebp-related protein 3).lim domain protein, cardiac (muscle lim protein) (cysteine-rich protein 3)	cardiac lim protein		Transcription Factor	
Msa.727.0	1.00	1.74	-5.46	1.82	-3.53	0.55	-5.48	1.18	-6.92	1.19	glutathione-S-transferase, alpha 3; Gsta3	M73483	glutathione S-transferase yc (ec 2.5.1.18) (gst class-alpha).	conjugation of reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles. this gst has a high catalytic activity for aflatoxin	9 48.0 cM	Metabolic	
Msa.27462.0	1.00	-1.46	-4.50	1.10	-4.40	1.47	-4.02	1.38	-7.09	1.40	growth hormone receptor; Ghr	AA066700	high molecular weight growth hormone receptor/binding protein precursor, low molecular weight growth hormone receptor/binding protein precursor	binding of gh to ghr activates insulin-like growth factor 1 (igf1), which in turn binds to its own receptor to activate signal-transduction pathways leading to growth	15 4.6 cM	Receptor	
Msa.540.0	1.00	1.21	-5.09	2.84	-1.82	0.51	-5.41	1.45	-7.23	1.37	gap junction membrane channel protein beta 4; Gjb4	M91443	gap junction beta-4 protein (connexin 31.1) (cx31.1).	one gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell	4 57.5 cM		

Table 1. Properties of tetranectin and plasminogen-binding protein (Tna)

Accession	1.00	-4.39	-3.08	2.24	-1.82	0.28	-7.10	3.28	-11.54	3.71	tetranectin (plasminogen-binding protein); Tna	X79199	tetranectin precursor (tn) (plasminogen- kringle 4 binding protein).	aka plasminogen binding protein -- a protein with a c-type lectin domain, is found in both serum and the extracellular matrix. it is a matricellular protein and plays a role in provides a release mechanism for internal cellular Ca^{2+} . mutation associated with human malignant hyperthermia (mh)(omim 1456). ryr1 is predominant in skeletal muscle, but is also detectable in heart and in brain	9 71.0 cM	ECM (Matrix Prot)	
X83932	1.00	2.28	-3.02	1.55	-0.27	1.54	-1.90	0.20	-15.56	13.50	ryanodine receptor 1; skeletal muscle; Ryr1	X83932			7 10.0 cM	Receptor	
M91602	1.00	-1.04	-6.76	4.34	-1.48	0.21	-18.83	7.24	-16.81	3.83	myosin light chain, phosphorylatable, cardiac ventricles; Mylpc	M91602	myosin regulatory light chain 2, ventricular/cardiac muscle isoform (mlc-2)	myosin regulatory light chain 2, ventricular/cardiac muscle		Structural Protein	
Msa.1007.0	1.00	1.20	-10.87	7.61	-1.90	0.38	-26.29	5.63	-17.28	4.06	myosin light chain, phosphorylatable, cardiac ventricles; Mylpc	M91602	myosin regulatory light chain 2, ventricular/cardiac muscle isoform (mlc-2)	a regulatory light chain predominantly expressed in ventricular cardiac muscle		Structural Protein	
M29793	1.00	1.28	-6.52	3.56	-2.79	0.98	-19.87	14.88	-18.50	9.76	troponin C, cardiac/slow skeletal; Tncc	M29793	troponin c, slow skeletal and cardiac muscles (tn-c).	troponin is the central regulatory protein of striated muscle contraction. tn consists of three components: tn-i which is the inhibitor of actomyosin atpase, tn- t which contain the binding site for tropomyosin and tn-c. the binding of tropomyosin	14 10.0 cM	Structural Protein	